

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 103887

TO: Vanessa L Ford

Location:

**Art Unit: 1645** 

Tuesday, September 16, 2003

Case Serial Number: 09596101

From: Edward Hart

**Location: Biotech-Chem Library** 

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

### Search Notes

Examiner Ford,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 



From:

Chan, Christina

Sent:

Monday, September 15, 2003 8:51 AM Ford, Vanessa; STIC-Biotech/ChemLib RE: In re:09596101 Sequence search

Subject:

#### Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Ford, Vanessa

Sent:

Saturday, September 13, 2003 5:15 PM

To:

Chan, Christina

Subject:

In re:09596101 Sequence search

Please search SEQ ID NO:1 and 3.

Please include interference searches. Please rush.

Vanessa L. Ford

**Biotechnology Patent Examiner** 

Office: CM1 8A16 Mailbox: CM1 8E12 Phone: 703.308.4735 Art Unit:1645

> Edward Hari Technical Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:	
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Date Picked Up: 7	14105
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TYPE OF SEARCH:
NA Sequences:
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VENDOR/COST (where applic.)	)
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Questel/Orbit:	
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Sequence Sys.:	
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Other (specify):	

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



### STIC SEARCH RESULTS

### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

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>	I am an examiner in Workgroup: Example: 1610
· >	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
,	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Cor	mments:

Proposition General Completed to insite Still (State of Chem) (State) (Milardine Insite of Chem)



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Novel human diagno
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Human full-length Wild type Apaf-1 p Human apoptotic pr	AAY49432 AAY97649 ABG65662	21 22 23	1194 1194 1194	56.2 56.2	3 6 6	43 44 45
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Drosophila melanog	ABB63493	22	665	•	39	23
Candida albicans	ABP73776	23	540		39	22
Trichoderma harzia	AAR88406	17	292	•	39	21
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Salmonella typhi	AAU38450	22	1380		40	18
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+	AAU34845	22	1342	٠	40	16
just -	ABG04194	22	8		40	15
	ABP29826	23	575		40	14
Streptococcus poly	ABP27730	23	575		40	13
Novel human diagno	ABG04189	22	501	•	40	
Novel human diagno	419	22	254	62.5	40	11
Propionibacterium	AAU45016	22	205		40	10

# ALIGNMENTS

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RESULT 1
AAY24915
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                                                                                                                                                                         Eisenia foetida; coelomic cytolytic factor 1; CCF-1; cancer; trypanosomal infection; bacterial infection; tumour therapy; inflammation; immunology.
                           WPI; 1999-385905/32.
                                             De Baetselier P;
                                                                                                                                                         Eisenia foetida.
                                                                                                                                                                                                              Eisenia foetida coelomic cytolytic factor 1 peptide
                                                                                                                                                                                                                                                    AAY24915;
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                                                               (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
                                                                                 17-DEC-1997;
                                                                                                    16-DEC-1998;
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Eisenia foetida polypeptides derived from coelomic cytolytic factor 1

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RESULT 2
AAY24914
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Best Local
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Claim 2; Page 48-49; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                     WO9931229-A2
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DB; AAX83611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF-alpha.
                                            from coelomic cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                              factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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XXX

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The present sequence represents the Elsenia foetida coelomic cytolytic factor 1 (CCF-1). The protein has antiparasitic, antibacterial and

A novel beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica

Claim 1; Page 42-43; 60pp;

English.

flavourings and yeast extracts

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RESULT 3
AAR97362
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333333333333333333XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (rCCF-1) is trypanolytic for the African trypanosome Trypanosoma brucei in a dose-dependent manner. The trypanolytic activity of rCCF-1 can be inhibited by anti-CCF-1 and anti-tumour necrosis factor (TNF)/TIP monoclonal antibodies. Furthermore, N,N'-diacetlychitobiose inhibits potently trypanolytic activity of rCCF-1. These data corroborate the findings that CCF-1 shares a trypanolytic, lectin-like domain with TNF-alpha. CCF-1 is useful to treat trypanosomal or bacterial infections or cancer. The proteins and peptides are also useful in tumour therapy, inflammation and other areas of immunology. The annelid peptide is derived from a 42 kba cytolytic protein named CCF-1 that binds lipopolysaccharide and beta-1,3-glucan. The factor resembles the
                                                  DNA construct encoding enzyme with beta-1,3-glucanase activity useful for modifying or degrading beta-glucan contg. material \langle the prepn. of e.g. food colourants, flavourings and yeast extra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                                                                              WPI; 1996-222000/22.
N-PSDB; AAT29043.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR97362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lipopolysaccharide and beta-1,3-glucan. The factor resembles the vertebrate tumour necrosis factor-alpha (TNF-alpha), and may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory activity. Recombinant coelomic cytolytic factor 1 (rCCF-1) is trypanolytic for the African trypanosome Trypanosoma bu
                                                                                                                                                         Savva
                                                                                                                                                                     Asenjo JA,
                                                                                                                                                                                                 (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                              14-OCT-1994;
                                                                                                                                                                                                                                                          16-0CT-1995;
                                                                                                                                                                                                                                                                                      25-APR-1996
                                                                                                                                                                                                                                                                                                                  WO9612013-A1
                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oerskovia xanthineolytica strain LLG109 (DSM 10297)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oerskovia beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR97362 standard; Protein; 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alternative for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
                                                                                                                                                         Ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SGEIDIIETIGNR 13
||||||||||||||
78 SGEIDIIETIGNR 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AA;
                                                                                                                                                                     Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                              94DK-0001192
                                                                                                                                                                                                                                                          95WO-DK00414
                                                                                                                                                                                                                                                                                                                                                           /label= Pro_peptide
                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                     Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF-alpha.
                                                                                                                                                                                                   AS
                                                                                                                                                                      Ferrer P,
                                                                                                                                                                                                                                                                                                                                             Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                    Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                      Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
0.00092;
                                                                                                                                                                      Hedegaard L;
                                                                   contg. material and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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В
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                                                                                               RESULT 4
AAB52463
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                               The present invention relates to Mycobacterium tuberculosis secreted proteins (MTSP), where the polypeptide has M. tuberculosis specific antigenic and immunogenic properties. Compositions of the invention be useful for diagnosing Mycobacterium tuberculosis infection and as vaccine against M. tuberculosis infection.
                                                                                                                                                                                         Claim 11; Fig 1; 60pp; English.
                                                                                                                                                                                                                      Novel Mycobacterium tuberculosis secreted polypeptides and polynucleotides useful in diagnosis, treatment and prophylaxis tuberculosis.
                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                        04-MAY-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLG109 is useful for degrading or modifying beta-glucan-contg. material. Its amino acid sequence was deduced from a genomic DNA sequence (AAT29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glucanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or Toc46. Protease-free beta-1,3-glucanase can be obtd. that is useful for lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the prodn. of pigments, colorants, flavours, yeast extract
                                                                                               Sequence
                                                                                                                                                                                                                                                                                         Gennaro
                                                                                                                                                                                                                                                                                                                                                                           04-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB52463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB52463 standard; protein;
                                                                                                                                                                                                                   tuberculosis
                                                                                                                                                                                                                                                                                                             (PUBL-) PUBLIC HEALTH RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                         WO200066143-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceuticals.
                                                                                                                                                                                                                                                                 2001-007151/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
  169
                                                                                                                                                                                                                                                                                         Ă,
                                                Similarity 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
9; Conser
SCEIDLIEWYGN 180
                     SGEIDIIETIGN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGEIDIMENVGN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGEIDIIETIGN 12
                                                                                             294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                         Gomez MJ;
                                                                                                                                                                                                                                                                                                                                                                         2000WO-US12197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                     99US-0132479.
99US-0132503.
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                                                          70.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB Pred. No. 0.33 2; Mismatches
                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                         Score 45; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                                NEW
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; MTSP; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein #28
                                                       DB
2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.33;
                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                 tuberculosis secreted
                                                                   Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 306;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                            of
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                        , тау
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SCEIDIIETIC

116 SCEIDIMENVG

126 11 Matches

Similarity 8; Conser

Conservative

18;

Indels

0,

Gaps

0

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RESULT 5
AAW29455
                                                                                This polypeptide comprises a novel Oerskovia xanthineolytica (OX)
enzyme that exhibits beta-1.3-glucanase (BG) activity. Its amino
acid sequence was deduced from an isolated genomic DNA sequence
(see AAR89155). Claimed DNA constructs that encode the novel BG (see
AAW29456 for corrected sequence), a mannose binding domain (see
AAW29456) or a full-length enzyme, i.e. BG with mannose binding
domain (see AAW29456), can be used to produce recombinant BG
polypeptides, with or without a mannose binding domain, in fungal
or bacterial host cells. BG polypeptides are used for the
degradation or modification of beta-glucan containing material,
especially for the gentle lysis of microbial cell walls, thereby
reduced amount of contaminants. They can also be used for the
production of e.g. pigments, colourants, flavourants, yeast
extracts, pharmaceuticals, food or feed compositions, and to
prepare protoplasts for use in fusion, transformation and cloning
              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                             New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for for obtaining desirable products
                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-526451/48.
                                                                                                                                                                                                                                                                                                     Example 2; Page 35-36; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                       Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-1,3-glucanase; lytic enzyme; yeast;
fungal cell wall; intracellular product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oerskovia xanthineolytica mature beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW29455 standard;
                                                                                                                                                                                                                                                                                                                                                                                    AAT89155
                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xanthineolytica
                                                  263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96DK-0000885
96DK-0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= k
164..952
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23..120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
             68.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Halkier

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLG109
Score 44; DB Pred. No. 3.9; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263
                                                                                                                                                                                                                                                                                                                                                                                                                      Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                      Hedegaard L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DSM 10297).

    obtained from Oerskovia
the lysis of microbial cells

          ДВ
3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta glucan degradation; purification; protoplast
                       Length 263;
                                                                                                                                                                                                                           (see
                                                                                                                                                                                                                                         (see
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RESULT 6
AAW29457
                                                                                                       밁
                     Q
                                                                                                                                                    cerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89157). Claimed DNA constructs that encode the novel BG (see also AAW29455), a mannose binding domain (see AAW29458) or a full-length enzyme, i.e. BG with mannose binding domain (see AAW29458), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal cor bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, cespecially for the gentle lysis of microbial cell walls, thereby cenabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the production of e.g. pigments, colourants, flavourants, yeast centracts, pharmaceuticals, food or feed compositions, and to
                                                               Query Match
Best Local
                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated beta-1,3-glucanase enzyme - oberathineolytica, used particularly for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-1,3-glucanase; lytic enzyme; yeast;
fungal cell wall; intracellular product;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oerskovia xanthineolytica beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW29457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW29457 standard;
                                                                                                       Sequence
                                                                                                                                         prepare protoplasts
                                                                                                                                                                                                                                                                                                                                             This sequence comprises the polypeptide precursor of a novel
                                                                                                                                                                                                                                                                                                                                                                       Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                               for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-526451/48
 169
                                                  Similarity
8; Conserv
SGEIDIMENVG
                        SCRIDITETIC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xanthineolytica LLG109 (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                      Page 42-43;
                                                                                                       303
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96DK-0000885
96DK-0000427
                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halkier
                                                                                                                                                                                                                                                                                                                                                                       64pp; English.
                                                                                                                                             use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303
                                                 Score 44; DB 1
Pred. No. 4.6;
2; Mismatches
                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hedegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta glucan degradation;
purification; protoplast
                                                                                                                                                                                                                                                                                                                                                                                                            obtained from Oerskovia
he lysis of microbial cells
                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ,
                                                  Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protoplast
                                                  0
                                                  Gaps
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RESULT 7
AAW29456
Query Match
Best Local S
Matches
                                                                                                                                                                                                               (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW2947), a MDB (see AAW29458), or the full-length enzyme can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oerskovia xanthineolytica beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW29456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29456 standard; Protein; 435
                                                                                                                                                                          production of e.g. pigments, colour extracts, pharmaceuticals, food or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated beta-1,3-glucanase enzyme - obxanthineolytica, used particularly for the for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oerskovia xanthineolytica LLG109 (DSM 10297).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast.
                                                                                                                                     studies
                                                                                                                                                          prepare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oerskovia xanthineolytica enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 39-40; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence comprises the polypeptide precursor of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997-526451/48.
8; Conserv
                                                                                                                                                       protoplasts for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrer P,
                                                                                           435
  Conservative
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                                                                                           β
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96DK-0000885
96DK-0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-DK00160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Mannose-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label = Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                         68.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sig_peptide
                                                                                                                                                            use
                                                                                                                                                          in
                       Score 44;
Pred. No.
                                                                                                                                                                               colourants, flavourants, yeast ood or feed compositions, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ħ,
                                                                                                                                                          fusion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that exhibits beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hedegaard
                                                                                                                                                            transformation and cloning
                                              DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obtained from Oerskovia
ne lysis of microbial cells
                                              18;
                                              Length 435;
       Indels
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    0;
    Gaps
       0;
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В QΥ

169

SGEIDIIETIG

11

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RESULT 9
ABG04199
ID ABG0
XX
AC ABG(
XX
DT 13-)
XX
DE NOV
XX
KW Hurr
KW Foc
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OS Hor
XX
PN WO
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PPN WO
XX
PPS 3(
XX
PR 3:
PR 3:
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XX
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                                                                                                                                                                                                                                                                                                                                       RESULT 8
AAB99272
                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 8
                                                                                                                 Human; chromosome mapping; gene ma
food supplement; medical imaging;
          31-MAR-2000;
23-AUG-2000;
                                       30-MAR-2001;
                                                           11-OCT-2001
                                                                             WO200175067-A2
                                                                                                 Homo sapiens
                                                                                                                                               Novel human diagnostic protein #4190
                                                                                                                                                                    13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                      The present sequence is beta-1,3-glucanase from Bacillus circulans. The protein can be used in various industrial fields such as stockbreeding, cake and bread manufacture and brewing.
                                                                                                                                                                                                                                                                                                                                                                                                                        Beta-1,3-glucanase and beta-1,3-glucan-binding peptide and their genes
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-364762/38.
N-PSDB; AAH46359, AA
                                                                                                                                                                                                          ABG04199 standard;
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2001120280-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEIJ ) MEIJI SEIKA KAISHA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus circulans beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB99272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB99272 standard; protein;
                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                           118
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                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                         SGEIDIMERVNN 129
                                                                                                                                                                                                                                                                             SGEIDIIETIGN 12
                                                                                                                                                                                                                                                                                                                                                                                             Page 8-9; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                       384 AA;
                                                                                                                                                                                                                                                                                                 Conservativé
          2000US-0540217
2000US-0649167
                                                                                                                                                                  (first entry)
                                      2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0311073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0311073
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH46360
                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme;
                                                                                                                                                                                                                                                                                                          67.2%;
                                                                                                                gene mapping; gene therapy; forensi
maging; diagnostic; genetic disorder
                                                                                                                                                                                                         185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stockbreeding; bread manufacture; brewing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384
                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                         Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋛
                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                 Length 384
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                              0;
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RESULT 10
AAU45016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
   21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                          20-APR-2001; 2001WO-US12865
                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                     WO200181581-A2
                                                                                                                                                                                                                                                                                                               Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                            dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes immunogenic protein #5912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU45016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU45016 standard; Protein; 205
                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID No 34558; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 GEVDDIDHLGNR 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS68386.
                                                                                                                                                                                                                                                                                                                                                                                                                                             endophthalmitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEIDIIETIGNR 13
; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      synovitis; acne; pustulosis; hypertosis; thalmitis; bone; joint; central nervous sysion; acne vulgaris; enzyme linked immuno;
                                                                                                                                                                                                                                                                                                                                                                         osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.5%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB
Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide (I) and
s useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 185
                                                                                                                                                                                                                                                                                                                                                                                                         immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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RESULT 11
ABG04191
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the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acnes in a particularly involved in the inflammatory cannot be presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by conzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogen polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-616774/71.
N-PSDB; AAS59524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW,
                                             31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                               30-MAR-2001; 2001WO-US08631
                                                                                                                                 11-OCT-2001.
                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #4182.
                                                                                                                                                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                        ABG04191;
                                                                                                                                                                                                                                                                                                                                                                                       ABG04191 standard; Protein;
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              (HYSE-) HYSEQ INC
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7; Conser
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58.3%;
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, Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                          254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB
Pred. No. 17;
3; Mismatches
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rter D;
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are used in
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RESULT 12
ABG04189
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating of disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of diagnostics, for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human contact of the invention.

Note: The sequence data for this patent did not appear in the printed sepecification, but was obtained in electronic format directly from WIPO as for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-2002
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                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome food supplement; m
                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                 11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                               (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic protein #4180.
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                                                                                                                                       2000US-0540217.
2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder.
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58.3%;
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Pred. No.
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CC Note: The sequence data for this pattent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fire the sequence data for this pattent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fire the sequence data for this pattent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fire the sequence of the content 
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Matches
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                                                                                                       27-OCT-2000; 2000GB-0026333
24-NOV-2000; 2000GB-0028727
07-MAR-2001; 2001GB-0005640
                                                                                                                                                                                                                                                                                                                                                          Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus polypeptide SEQ
    Telford J,
                                         (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC
                                                                                                                                                                                          29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                      02-MAY-2002.
                                                                                                                                                                                                                                                                                WO200234771-A2
                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP27730 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 34548; 103pp; English
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DB; AAS68376.
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    Masignani V,
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58.3%;
  Margarit Ros
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Pred. No. 48;
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ΥI,
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RESULT 14
ABP29826
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CC (Streptococcus/GBS), comprising one of 5483 sequences ($1), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), nucleic acids encoding (I), ABN6604-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC treptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by CC Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity CC Streptococcus proteins and distinguishing/identifying CC Streptococcus proteins and selections and distinguishing/identifying CC Streptococcus proteins and selection an
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Best Local :
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                                                                                                                                                                      27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                         (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
WPI; 2002-352536/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ
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                                                             Telford
                                                                                                                                                                                                                                                             29-OCT-2001; 2001WO-GB04789.
                                                                                                                                                                                                                                                                                                           02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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                                  ។ J,
។ H;
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INST GENOMIC RES
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8; Conserv
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                                                           Masignani V,
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; 2000GB-0028727.
; 2001GB-0005640.
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66.7%;
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RESULT 15
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Matches 8
           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS68381.
                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                   11-OCT-2001.
                                                                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG04194 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
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2000US-0649167.
                                                                                                                                     Liu C,
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Search completed: September 16, 2003, 11:25:53 Job time: 4.96222 secs
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Best Local Similarity
"~+~hes 7; Conserv:
                                                                                                                                                                                                                                                                                                                     CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical conditions of the separating of sites expressing (II). (I) and (II) are useful for treating CC disgraphing of sites expressing (II). (I) and (II) are useful for treating CC disgnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess blodiversity amino acid sequences of the invention.

CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30373 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cast first who, with the souther content of creat directly from WIPO at frequency.
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and
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                                                                                                     GEVDDIDHLGNR
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58.3%;
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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Match
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/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/BCTUS_COMB.pep:*
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US-08-712-072C-3
US-09-092-508-2
US-09-092-508-2
US-09-092-508-16
US-09-08-310-2
US-09-08-310-2
US-09-08-310-2
US-09-252-991A-25247
US-09-252-991A-25247
US-09-353-352-6383
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US-08-36-063-44
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US-09-137-440-44
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US-09-159-106-11
US-09-266-225D-12
US-09-328-352-8132
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Query Match Best Local S Matches 9

Similarity 75. 9; Conservative

78.1%;

Score 50; DB 2 Pred. No. 0.15; Mismatches

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Length 306; Indels

0;

Gaps

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; MOLECULE TYPE: protein US-08-824-707-2

COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURENT APPLICATION DATA: APPLICATION NUMBER: US/08/824,707 FILING DATE: 14-April-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Gregg, Valeta A. REFERENCE/DOCKET NUMBER: 4290.204-US TELEPHONE: 212-867-0123 TELEPHONE: 212-878-9655 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 306 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: brottein	RESULT 1 US-08-824-707-2 US-08-824-707-2 Sequence 2, Application US/08824707 Patent No. 5919688 ; GENERAL INFORMATION: APPLICANT: Ferrer, Pau APPLICANT: Diers, Ivan APPLICANT: Hedegaard, Lisbeth APPLICANT: Hedegaard, Lisbeth APPLICANT: Asenjo, Juan APPLICANT: Savva, Demitris TITLE OF INVENTION: No. 5919688el enzyme with beta-1,3 NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSE: No. 59196880 No. 5919688disk of No. 59196 STREET: 405 Lexington Avenue, Suite 6400 CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10174-6401	28 35 54.7 746 4 US-09-252-991A-18587 29 35 54.7 1151 4 US-09-252-991A-21328 30 34.5 53.9 448 4 US-09-252-991A-21328 31 34 53.1 141 4 US-09-328-352-6280 32 34 53.1 141 4 US-09-632-991A-22440 33 34 53.1 342 4 US-09-632-947B-22 34 34 53.1 342 4 US-09-632-991A-25366 35 34 53.1 582 4 US-09-457-046B-63 35 34 53.1 654 1 US-08-392-828C-2 37 34 53.1 654 1 US-08-392-828C-2 38 34 53.1 1119 3 US-09-396-651B-2 39 34 53.1 1119 3 US-09-396-651B-2 40 33 51.6 278 4 US-09-252-991A-27917 41 33 51.6 278 4 US-09-252-991A-27917 42 33 51.6 280 4 US-09-053-374A-5 43 33 51.6 386 4 US-09-053-374A-5 44 33 51.6 394 1 US-08-018-489C-5 45 33 51.6 394 1 US-08-018-489C-5
	-1,3-glucanase activity 919688th America, Inc:	Sequence 18587, A Sequence 21043, A Sequence 221043, Ap Sequence 27440, A Sequence 27, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7679, Ap Sequence 7679, Ap Sequence 5, Appli

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TITLE OF INVENTION: An Enzyme With -1,3-Glucanase
TITLE OF INVENTION: Activity
FILE REFERENCE: 4693.204-US
CURRENT APPLICATION UNMEER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER FILING DATE: 1996-12-04
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1997-04-14
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TITLE OF INVENTION: Activity
FILE REFERENCE: 4693 204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER FILING DATE: 1996-08-596
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
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LENGTH: 303
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SOFTWARE: FastSEQ for
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APPLICANT: Hedegaard, Lisbeth
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APPLICANT: Diers, Ivan
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\PPLICANT: Diers, Ivan
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FILE REFERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/266,225D CURRENT FILING DATE: 1999-03-10 NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 816
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                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09266225D Patent No. 6573364
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                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-TITLE OF INVENTION: Interacting Proteins FILE REFERENCE: 15966-523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: PCT/DK97/00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisb
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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 54 EYEIIETIGN 63
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Tchernev, Velizar
                                                                Conservative
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80.0%;
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Pred. No.
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Pred. No.
                                                                Mismatches
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RESULT 7
US-08-712-072C-4
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-8132
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APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08712072C Patent No. 5925541
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Best Local
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Patent No. 6562958
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                                                                                                                                                                                        TELEPHONE: (212) 697-5995
TELEPAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acid
                                                                                                                                                                                                                                                             NAME: Bogosian, Elizabeth A.
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/712,072C
                                                    HYPOTHETICAL: |
                                                                                     MOLECULE TYPE:
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MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
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ORGANISM: gub,
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ADDRESSEE: Ams...,
ADDRESSEE: Ams...,
                                                                                                                     STRANDEDNESS:
                                                                                                                                         TYPE: amino acid
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STATE: NY
                                                                                                       TOPOLOGY:
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 Rhodothermus marinus
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58.3%;
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Pred. No.
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                                                                Patent No.
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GENERAL IN
                                                                           Sequence 4,
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                Query Match
                         GENERAL INFORMATION:
APPLICANT: Kofod,
APPLICANT: Anderse
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Best Local :
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LENGTH: 292 amino acids
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase TITLE OF INVENTION: Activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212-878-9655
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01
FILING DATE: 08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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                                                                                                                                         158 GEIDIMETV 166
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5. 5871966
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                                                                , Application US/09098580
6140096
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Christgau, Stephan
         Kofod, Lene Venke
Andersen, Lene No. 61400
Anuppinen, Markus Sakari
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Kauppinen, Markus Sakari
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77.8%;
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for Windows Version
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63.6%;
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Pred. No.
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Pred. No.
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20691
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APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                    Query Match
                                                                                                                       SEQ ID NO 20691
LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                            Sequence 20691, Ap
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
       Matches
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                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,580
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/7
FILING DATE: 08-NOV-1996
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
08/737,526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                      Local Similarity
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Local Similarity 77.8%;
es 7; Conserva++...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Valeta, Gregg A REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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|158 GEIDIMETV 166
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     Conservative
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1998-02-18
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                   50.9%;
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                 Score 39; DB 4;
Pred. No. 35;
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Pred. No. 16;
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     Mismatches
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RESULT 12
US-09-330-945-37
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US-08-392-828C-37
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                        Sequence 37, Appli
Patent No. 6077946
GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01
FILING DATE: 28-FEB-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                LOCATION: 1..262
OTHER INFORMATION: /note= "BG1 A1 SEQUENCE (FIGURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: BOSTON
                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                          |||||::| |
130 SGEIDVMEARG 140
                           INFORMATION:
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                                                                                                                                                    1 SGEIDIIETIG 11
                                                                                                                                                                               Similarity 7; Conserv
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                                                     Application US/09330945
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MUTA, TATSUSHI
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SEKI, NORIAKI
            IWANAGA, SADAAKI
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Pred. No.
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TITLE OF INVENTION:

SEKI, NORIAKI ODA, TOSHIO VENTION: DNA ENCODING HORSESHOE CRAB

0,;

APPLICANT:

11-SEP-1996

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RESULT 13
US-08-712-072C-3
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Best Local
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APPLICANT: Jack Gold
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                             STREET: >U
STREET: NEW YORK
CITY: NEW YORK
CMATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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                                                                                                                                                     ADDRESSEE: Allocation Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COTHER INFORMATION: /note= "BG1 A1 SEQUENCE (FIGURE 2)"
                                                OPERATING SYSTEM: MS-DOS
                                                                COMPUTER:
                                                                                                                           COUNTRY: US
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,072C
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                             130 SGEIDVMEARG 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                               Jack Goldstein, Alex Zhu and Lin Leng
VENTION: ENDO-BETA-GALACTOSIDASE
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                                                             IBM PC COMPATIBLE
                                                                                                                                                                                     Amster, Rothstein & Ebenstein
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63.6%;
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RESULT 14
US-09-092-508-2
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; ORIGINAL SOURCE:
; ORGANISM: e131
US-08-712-072C-3
                                                                            FILING LALE.

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/048,807

FILING DATE: 05-JUN-1997

APPLICATION NUMBER: 60/055,258

APPLICATION NUMBER: 07-AUG-1997

TYTING DATE: 07-AUG-197
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TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                        FILING DATE: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Ph.D., Denise M
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                        ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                SOFTWARE: FastSEQ for Wilcurrent Application DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 05-JUN-1998
TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Henzel, William J. TITLE OF INVENTION: APAF-1, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Minneapolis
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63.6%;
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US-09-435-115-2
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US-09-092-508-2
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Patent No. 6346607
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/055,258
FILING DATE: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, ph.D., Denise M
RECISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11669.6USU1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Henzel, William J.
APPLICANT: Henzel, William J.
TITLE OF INVENTION: APAF-1, AN ACTIVATOR OF C ASPASE-3
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6346607west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 56.2%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LIBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/435,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                     TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                   LENGTH:
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STRANDEDNESS: single
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Pred. No. 2.9e+02;
4; Mismatches 3; Indels
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Pred. No. 2.9e+02;
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Search completed: September 16, 2003, 11:30:24 Job time: 2.37531 secs

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22-Oct-1999

Harris, D.;

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Perfect score:
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Copyright (c) 1993 - 2003
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(without alignments)
763.579 Million cell updates/sec
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A;Cross-references: GB:U49711; NID:g1488256; PIDN:AAC47235.1; PID:g1488257
A;Accession: PC6037
A;Molecule: type: protein
A;Residues: 21-40;197-209;329-344 <BA2>
A;Experimental source: egg
C;Comment: This enzyme functions in several extracellular activities inclusefense enzymes in plants.
C;Keywords: egg; glycosidase; hydrolase
                                                                                                                                                                 R;Bachman, E.S.; McClay, D.R.
Proc. Natl. Acad. Sci. U.S.A. 93, 6808-6813, 1996
A;Title: Molecular cloning of the first metazoan beta-1,3
A;Reference number: JC6141; MUID:96270625; PMID:8692900
A;Accession: JC6141
                                                                                                                                                                                                                                                  beta 1,3-glucanase (EC 3.2.1.-) precursor - sea urchin (Strongylocentrotus purpuratus C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 21-Jul-2000 C;Accession: JC6141; PC6037
                                                                                                                                                                                                                                                                                                                      RESULT
JC6141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; I Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Mycobacterium tuberculosis C; Date: 17-U1-1998 #sequence_revision C; Accession: D70525
                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-499 <BAC>
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strain H37Rv
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75.0%;
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DB 2;

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RESULT
E87311
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C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
C;Dates: 009-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
C;Accession: JC7869; Pc7199
R;Asano, T; Taki, J; Yamamoto, M.; Aono, R.
Biosci. Biotechnol. Biochem. 66, 1246-1255, 2002
B;Title: Cloning and structural analysis of bglM gene coding for the fungal A;Reference number: JC7869; MUID:22152179; PMID:12162545
A;Accession: JC7869
                                                                                                        8
                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 28-42;95-111;152-170 <AS2>
C;Comment: This protein that is a fungal cell wall-degrading enzyme,
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A;Accession: PC7199
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A; Residues: 1-301 <STO>
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87296
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-411 <ASA>
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Accession: C87296
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8; Conserv
                                                                        SGEIDIMERVNN 156
                                                                                                            SGEIDIIETIGN 12
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ct: beta 1,3-glucanase #status predicted <MAT>
                                                                                                                                               Conservative
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66.7%;
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                                                                                                                                                              Pred. No. 5
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Pred. No. 2.
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Pred. No.
                                                                                                                                               Mismatches
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5.5;
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2.5;
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2.9;
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                                                  ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                     R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.;
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             ster, E.W.
                               A; Authors: Yoo, H.; Tao,
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The

Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58

P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kar

; Chen, L.; Kutyavin, T

Wood, G.E.; Chen,
T.; Levy, R.; Li,

MCC.

Y.; Biddle,

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A; Map position: I
C; Superfamily: DNA-directed RNA polymerase beta chain
C; Keywords: nucleotidyltransferase
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A;Residues: 1-1377 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51930.1; PID:g17982686; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melii A;Reference number: AD3252; PMID:11756888
A;Accession: AG3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA-directed RNA polymerase (EC 2.7.7.6) [imported] -C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #te
C;Accession: AG3345
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87311
DNA-directed RNA polymerase beta chain [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AB2817
                                                                                                AB2817
                                                                                                                         RESULT 7
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A; Residues: 1-1356 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005673; NID:g13421681;
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Best Local s
Matches 8
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Pred. No.
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21;
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                                                                     (strain
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R;Quetier, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; submitted to the Protein Sequence Database, April 1999
A;Reference number: 215794
A;Accession: T06757
A;Molecule type: DNA
A;Residues: 1-736 <QUE>
A;Cross-references: EMBL:ALO49660; GSPDB:GN00061; ATSP:F15B8.180
A;Experimental source: cultivar Columbia; BAC clone F15B8
C;Genetics:
A;Gene: ATSP:F15B8.180
A;Map position: 3
A;Introns: 114/3; 146/1; 208/2; 293/3; 365/3; 384/3; 429/3; 467/3
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A;Accession: C97595
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C97595
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A;Accession: AB2817
A;Status: preliminary
A;Molecule type: DNA
A,Residues: 1-1378 (KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42952.1; PID:g1:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rpoB
A;Map position: circular chromosome
C;Superfamily: DNA-directed RNA polymerase beta chain
                                                                                                                                                                                                                                                                                                                              hypothetical protein F15B8.180 - Arabidopsis thaliana C;SpecLes: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change C;Accession: T06757
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A; Map position: ci:
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A:Molecule type: DNA
A:Residues: 1-1411 <KUR>
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A.; Liu, F.; Wollam, C.; Allinger, M.;
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA polymerase beta chain (AF171070) [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: C97595
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De: Cultivar Columbia; BAC clone F15B8
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72.78;
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Doughty, D.; Scott, C.; Lappas, C.;
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ckelz, B.;
                                                                                                                                                                                                                                                                                                             Mewes,
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RNECE
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Escherlchia Cult Nichlternate names: transcriptase beta chain
C;Species: Escherichia coli
C;Bate: 31-Oct-1980 #sequence_revision 12-Dec-1997 #text_change 01-Mar-2002
C:Accession: F65205; A91109; JN0244; S12576; A91472; A00689; I52540; I52542;
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                                                                                                                                         RESULT 12
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A; Neuron : DNA
A; Molecule type: DNA
A; Residues: 1-1302 < LAI>
A; Cross-references: EMBL: U25815; NID: 9886051; PID: 9886053;
A; Cross-reference: strain R8A2HP; specific_host Citrus
                                                                                                                                                                                                                                                                                                     R:Laigret, F.; Gaurivaud, P.; Bove, J. Gene 171, 95-98, 1996
A;Title: Unique organization of the rpoB region of Spiroplasma A;Reference number: Z22353; MUID:96257200; PMID:8675039
A;Accession: T43230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: ATP
F;52-315/Domain: protein kinase homology <KIN>
F;60-68/Region: protein kinase ATP-binding motif
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B56708
                                                                                                                                  C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Spiroplasma citri
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 270, 12665-12669, 1995
A;Title: Components of a new human protein
A;Reference number: A56708; MOID:95279403;
A;Accession: B56708
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C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995
                                                                                                                                                                    A; Genetic
                                                                                                                                                                                                                                                                                     A; Status: preliminary;
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A; Residues: 1-815 <ZHO>
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8; Conserv
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PMID:7759517
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A; Molecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-105, 'G', 108-383, 'CSRTCSSP' <DEL>
A; Cross-references: GB: V00341; NID: g42823; PIDN: CAA23629.1;
R; Gurevitch, A.I.; Avakov, A.E.; Kolosov, M.N.
Bloorg. Khim. 5, 1735-1738, 1979
A; Title: The nucleotide sequence at the proximal end of rpoB
A; Reference number: A00689
A; Status: significant sequence differences
A; Status: significant sequence differences
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A;Title: Nucleotide sequence of the proximal portion of A;Reference number: A91472; MUID:81165543; PMID:7011900 A;Accession: A91472
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A;Residues: 1-515,'V',517-1342 <OVC>
A;Residues: 1-515,'V',517-1342 <OVC>
A;Cross-references: GB:V00339; GB:J01678; GB:K00449; NID:g42813; PIDN:CAA23625.1;
A;Note: most of this sequence was confirmed by amino acid analysis
A;Ovchinnikov, Y.A.; Sverdlov, E.D.; Lipkin, V.M.; Monastyrskaya, G.S.; Chertov, C
A;Molecule type: DNA
A;Residues: 187-354 (RE2)
A;Cross-references: GB:M38304; NID:g147719;
R;Gurevich, A.I.; Igoshin, A.V.; Kolosov, M.
Bioorg. Khim. 6, 1580-1584, 1980
                                                                                                                      A;Cross-references: GB:M38292; NID:g147717; PID R;Sverdlov, E.D.; Lipkin, V.M.; Monastyrskaya, Bioorg. Khim. 6, 309-312, 1980
A;Title: The nucleotide sequence of strong RNA A;Reference number: I52542
A;Accession: I52542
A;Status: preliminary; translated from GB/EMBL/
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R;Post, L.E.; Strycharz, G.D.; Nomura, M.; Lewis, H.;
Proc. Natl. Acad. Sci. U.S.A. 76, 1697-1701, 1979
A;Title: Nucleotide sequence of the ribosomal protein
A;Reference number: S12572; MUID:79201667; PMID:377281
A;Accession: S12576
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                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-188 < RES>
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Bioorg. Khim. 6,
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Gene 11, 367-373,
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A;Reference number: JN0244
A;Accession: JN0244
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A; Title: The primary structure of Escherichia coli RNA |
A; Reference number: A91109; MUID:81260785; PMID:6266829
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A;Cross-references: GB:AE000472; GB:U00096; NID:g2367333; PIDN:AAC76961.1; PID:g1790419; A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
R;Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Gubanov, V.V.; Guryev, S.O.; Chertov, O.Y.; M
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Science 277, 1453-1462, 1997
A;Title: The complete genome
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A; Residues: 1-33 < POS>
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                                                                                                                                                                                                                                                 PIDN:AAA24579.1; PID:g147718 ya, G.S.; Gubanov, V.V.; Gury
                                                PIDN: AAA24580.1;
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                                                PID:g551832
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                                              R;Lisitsyn, N.A.; Monastyrskaya, G.S.; Sverdlov, E.D. Eur. J. Blochem. 177, 363-369, Title: Genes coding for RNA polymerase beta subunit in A;Reference number: S01794; MUID:89052707; PMID:3056723
                                                                                                                 C;Species: Salmonella typhimurium
C;Date: 31-Dec-1990 #sequence_revision
C;Accession: S01794
R;Lisitsyn, N.A.; Monastyrskaya, G.S.;
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                         A; Reference number: A; Accession: S01794
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  A; Molecule type:
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C; Species: Buchnera aphidicola
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10
C; Accession: $32680
R; Clark, M.A.; Baumann, L.; Baumann, P.
submitted to the EMBL Data.Library, April 1992
A, Description: Sequence analysis of an aphid endosymbiont DNA fragrammer: $32679
A; Reference number: $32679
A; Accession: $32680
A; Molecule type: DNA
A; Residues: 1-1342 <CLA>
A; Cross references: EMBL:Z11913; NID:9296967; PIDN:CAA77970.1; PID
C; Superfamily: DNA-directed RNA polymerase beta chain
C; Keywords: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: rpoB
A;Map position: 90 min
C;Complex: the active enzyme consists of the sigma chaeleased; the core enzyme is composed of two alpha chaic;Function:
A;Description: part of the catalytic component of the C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Primary structure of EcoRI-F fragment of A;Reference number: I52539
A;Accession: I52539
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1143-1342 <RE4>
A;Cross-references: GB:M38293; NID:g147721; PIDN:AC;Genetics:
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A;Accession: I52541
A;Status: translated from GB/EMBL/DDBJ
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Bioorg. Khim. 6, 1106-1109, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M38303; NID:g147724; PIDN:AAA24583.1; R;Monastyrskaya, G.S.; Gubanov, V.V.; Guryev, S.O.; Lipkin, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1143-1342 <RE3>
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31-Dec-1990

bacteria.

Structure/function

beta

chain -

Salmonella typhimurium

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RESULT 15
F91242
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91242
Search completed: September 16, 2003, 11:29:36
Job time: 3.63728 secs
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C;Superfamily: DNA-directed RNA polymerase beta chain
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A;Molecule type: DNA
A;Residues: 1-1342 <HAY>
A;Residues: 1-1342 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB38333.1; PID:g13364386; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C; Superfamily: DNA-directed RNA polymerase beta chain
C; Keywords: nucleotidyltransferase; transcription
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A;Cross-references: GB:X04642; GB:M37431; GB:X04860; GB:X13854; NID:g47918; PIDN:CAA283
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Copyright (c) 1993 - 2003 Compugen Ltd
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RPOB_BCOLI
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RPOB_COADA
RPOB_PORPU
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E13B_BACCI
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Q13164 homo sapien
P47767 spiroplasma
P57146 buchnera ap
P41184 buchnera ap
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P00575 escherichia
P06173 salmonella
P43738 haemophilus
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MEDIJINE-99319892; PubMed=10392721;

MEDIJINE-99319892; PubMed=10392721;

Bahr U., Springfeld C., Tidona C.A., Darai G.;

Bahr U., Springfeld C., Tidona C.A., Darai G.;

Bahr U., Springfeld C., Tidona C.A., Darai G.;

"Structural organization of a conserved gene cluster of Tupaia

herpesvirus encoding the DNA polymerase, glycoprotein B, a probable processing and transport protein, and the major DNA binding protein.";

Processing and transport protein, and the major DNA binding protein.";

Virus Res. 60:123-136(1999).

-i- FUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION OF THE VIRUS

-i- FUNCTION: THIS PROTEIN MAY AFFECT TRANSLOCATION MATURATION
                                                                                                                                                                                               10-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase 7 (EC 2.7.1.-)
regulated kinase 5) (ERK-5) (BMK1 kinase).
MAPK7 OR ERK5.
                                                                                                                                                                                                                                                                              MK07_MOUSE
Q9WVS8;
            Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MEKS AND ERKS INTERACT SPECIFICALLY WITH ONE
-I- NOT WITH MEKL/ERK1 OR MEKZ/ERK2 PATHWAYS (BY SIMILARITY
-i- ENZYME REGULATION: Activated by tyrosine and threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01366; PRTP;
Capsid assembly.
SEQUENCE 782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                          Kamakura S., Moriguchi T., Nishida E.;
"Activation of the protein kinase ERK5/BMK1
kinases: identification and characterization
                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF084543; AAD42934.1; -
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Betaherpesvirinae.
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Viruses; dsDNA viruses,
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SIMILARITY: BELONGS TO THE HERPESVIRUSES
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phosphorylation
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Sciurognathi;
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MGD: MGD: 1346347; Mapk7.
GO; GO:0045765; P:regulation of ang
InterPro; IPR003527; MAP_kin.
InterPro; IPR000719; ProC_kinase.
InterPro; IPR002290; Ser_thr_pkinas
Pfam; PF00069; pkinase; 1
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DOMAIN 55
DOMAIN 434
DOMAIN 521
DOMAIN 578
NP_BIND 61
BINDING 84
ACT_SITE 182
MOD_RES 219
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PROSITE; PS001351; MAPK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS00108; PROTEIN_KINASE_DM;

PROSITE; PS50011; PROTEIN_KINASE_DM;
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SMART; SM00220; S_
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HSSP; P24941; 1H
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                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUTHE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE, WHICH COULD HAVE A RESIDUAL PART OF THE KINASE PART OF THE PART OF THE KINASE PART OF THE 
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BELONGS TO THE SER/THR FAMILY OF
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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RESULT
MK07_HU
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TISSUE-Fetal brain;
MEDLINE-95279403; PubMed-7759517;
Zhou G., Bao Z.Q., Dixon J.E.;
                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                          [1]
SEQUENCE FROM
                                                                                                 NCBI_TaxID=9606;
                                                                                                                        Primates;
                                                                                                                                           Chordata;
                                                                                                                        Catarrhini;
                                                                                                                                           Craniata; Vertebrata;
                                                                                                                                                                                                                        ion update)
(EC 2.7.1.-)
                                                                                                                                                                                                     (BMK1 kinase)
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                                                                                                                          Hominidae;
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Euteleostomi; Homo

RRY RAY

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Query Match
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EMBL; U29725; AAA82931.1;
EMBL; U29726; AAA82932.1;
EMBL; U29727; AAA82933.1;
PIR; B56708; B56708.
HSSP; P24941; 1HCL.
Genew; HGNC:6880; MAPK7.
                                                                                                                          Phosphorylation.
54
DOMAIN 337
DOMAIN 433
DOMAIN 520
DOMAIN 57
NP_BIND 60
BINDING 83
ACT_SITE 181
                                                                                                                                                                                                                                                                                                                                         GO; GO:0004707; F:MAP kinase activity; GO; GO:0007165; P:signal transduction; InterPro; IPR003237; MAP_kin.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee J.-D., Olevitch R.J., Han J.;
Primary structure of BMK1: a new mammalian map kinase.";
Biochem. Biophys. Res. Commun. 213:715-724(1995).
-I- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS.
-I- ENZYME REGULATION: Activated by tyrosine and threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathway."
J. Biol.
[2]
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                                      CONFLICT
                                                              CONFLICT
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ProDom; PD000001; Prot_kinase;
SMART; SM00220; S_TKC; 1.
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                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                             PROSITE; PS01351; MAPK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Components of a new human protein kinase signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. PW: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
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SIMILARITY: BELONGS T
MAP KINASE SUBFAMILY.
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                                                                                        220
                                                               19
                                                                                                                                                                                                                                          Serine/threonine-protein kinase;
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  62.5%;
 Score
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                                                            PHOSPHORYLATION (ACTIVATES (BY SIMILARITY).
AREGRIRPHRCLCS -> GPVKVEPAH
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                                                                                                                                          ATP
                                                                                                                                                      PRO-RICH 2.
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POLY-ARG.
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Length 815
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RESULT 6
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Matches 7
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Matches 8; Conser
                                                                                                                                                                               HSSP; 09KWU7; 1HQM.
InterPro; IPR001572; RNA_pol_B.
InterPro; IPR001572; RNA_pol_Rpb2_1; 1.
Pfam; PF04563; RNA_pol_Rpb2_2; 2.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF04565; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_POL_Rpb2_7; 1.
PR0SITE; PS01166; RNA_POL_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The unique organization of the rpoB region restriction and modification system gene is gene 171:95-98(1996).
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P47767;
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                             EMBL; U25815; AAC44217.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-R8A2HP;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the RNA polymerase beta chain family
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SUBUNIT: THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBSTRATES.
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. 33, Last sequence update)
. 37, Last annotation update)
. 37, Last annotation (EC 2.7.7.6) (Transcriptase polymerase beta subunit).
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47;
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RPOB_BUCAP
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DE DNA-d1
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Best Loc
Matches
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R HSSP; Q9KW07; 1HQM.

RICHEPTC; IPR001572; RNA_pol_B.

Pfam; PF04563; RNA_pol_Rpb2_1; 1.

Pfam; PF04561; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_6; 1.

Pfam; PF04560; RNA_pol_Rpb2_7; 1.

Pfam; PF04560; RNA_pol_Rpb2_7; 1.

Pfam; PF04560; RNA_pol_BETA; 1.

PFORSITE; PS01166; RNA_POL_BETA; 1.

PGOSTERS; PS01166; RNA_POL_BETA; 1.

PGOSTERS; PS01166; RNA_POL_BETA; 1.

PGOSTERS; PS01166; RNA_POL_BETA; 1.

PGOSTERS; PS01166; RNA_POL_BETA; 1.
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STRAIN=TOKYO 1998;
MEDLINE-20445173; PubMed=10993077;
MEDLINE-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y.,
Shigenobu T. The endocellular bacterial symptomic of the endocellular bacterial symptomi
                                                                                                                    RAPOB_BUCAP STANDARD; PRT; 1342 AA.

P41184;
01-FEB-1995 (Rel. 31, Created)
01-FEB-2003 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta for in the companion of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P57146;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                   Buchnera aphidicola (subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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NATURE 407:81-86 (2000).

-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta chain) (RNA RPOB OR BU034.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last anotation updat
DNA-directed RNA polymerase beta chain (EC
                                                             Bacteria; Proteobacteria;
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Enterobacteriaceae; Buchne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the RNA polymerase beta chain family.
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SUBUNIT: THE
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CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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58.3%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
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symbiont of
                                                      Enterobacteriales;
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RESULT 8
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Best Local
                                                                                                                   RPOB_ECOLI STANDARD: PRT; 1342 AA. p00575; p00576; p78242; 21-JUL-1986 (Rel. 01, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) DNA-directed RNA polymerase beta Chain (EC 2.7.7 beta chain) (RNA polymerase beta subunit). RPOB OR GRON OR NITB OR RIF OR RON OR STL OR STV C4944 OR Z5560 OR ECS4910 OR SF4060.
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PIR; S32680; S32680.

HSSP; OSKU07; HROM.

InterPro; IPRO01572; RNA_pol_B.

Pfam; PF04561; RNA_pol_Rpb2_1; 1.

Pfam; PF04561; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_3; 1.

Pfam; PF04565; RNA_pol_Rpb2_7; 1.

Pfam; PF04560; RNA_pol_Rpb2_7; 1.

Pfam; PF04560; RNA_POL_RPb2_7; 1.
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SEQUENCE
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                                               Escherichia coli 06,
Escherichia coli 0157:H7,
                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
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MEDLINE=93160925; PubMed=1369199;
Clark M.A., Baumann L., Baumann P
                                                                                                   Escherichia coli,
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                          Shigella
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[1]
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SEQUENCE FROM N.A.

SPECIES-E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasser D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpa Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Fortbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Pc Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Pc Grotbeck E.J., Anantharaman T.S., Lin J., Yen G., Schwar
                                                                                                                                                                                                  SEQUENCE FROM N.A.

SPECIES-E.coll; STRAIN=0157:H7 / RIMD 0509952;

MEDLINE-21156331; PubMed-11258796;

MEDLINE-21156331; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-E. coli; STRAIN=06:H1 / CFT073 / ATCC 700928;

SPECIES-E. coli; STRAIN=06:H2471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mohley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                              Welch R. "Genome
SEQUENCE OF 1-391
SPECIES=E.coli;
MEDLINE=81165543;
                                                                                                                                                                                                                                                                                                                                                              Nature
[6]
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Ovchinnikov Y.A., Monastyrskaya G.S., Gubanov V.V., Guryev S.O.,
Chertov O.Y., Modyanov N.N., Grinkevich V.A., Makarova I.A.,
Marchenko T.V., Polovnikova I.N., Lipkin V.M., Sverdlov E.D.;
"The primary structure of Escherichia coli RNA polymerase. Nucleotide sequence of the rpoB gene and amino-acid sequence of the
                                                                                                                             SPECIES=E.coli;
MEDLINE=79201667; PubMed=377281;
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SPECIES-E.coli; STRAIN-B;
Miller E.S., Shih G.C., Chung
Submitted (NOV-1996) to the Ex
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SPECIES-E.coli; STRAIN-K12 / MG1655;
MEDLINE-94089392; PubMed-8265357;
Blattner F.R., Burland V.D., Plunket
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                                                            Post L.E., Strycharz G.D., Nomura M., Lewis H., "Nucleotide sequence of the ribosomal protein ge to the gene for RNA polymerase subunit beta in E Proc. Natl. Acad. Sci. U.S.A. 76:1697-1701(1979)
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409:529-533(2001).
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8:11-22(2001).
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   PubMed=7011900
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EMBL/GenBank/DDBJ
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                                                                             gene cluster
n Escherichia
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, Kirkpatrick H.A.,
hao Y., Miller L.,
E.T., Potamousis K.,
, Schwartz D.C.,
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Lee J., Kashlev M., Borukhov S., Goldfarb A.;

"A beta subunit mutation disrupting the catalytic function of Escherichia coli RNA polymerase.",

Proc. Natl. Acad. Sci. U.S.A. 88:6018-6022(1991).

-j. FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y.,
Yang J., Yang F., Zhang X., Zhang J., Yar
Sun L., Xue Y., Zhao A., Gao Y., Zhu J.,
Cheng H., Yao Z., He B., Chen R., Ma D.,
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*Structure of a central part of E.coli ope 

sequence of the gene for beta subunit of R 

Bioorg. Khim. 6:1580-1584(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of RNA polymerase from of the rpoB gene fragment and correspondin sequence of the beta-subunit."; . Bioorg. Khim. 6:1423-1426(1980).
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"The nucleotide sequence
Escherichia coli.";
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[9]
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Mollet C., Drancourt M., Raoult
"RNA polymerase beta-subunit.";
submitted (NOV-1996) to the EMBI
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                                                                                                                                                                        MEDLINE=91296752; PubMed=2068078;
                                                                                                                                                                                                                                                                                                                                                                                       Yu J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-S.flexneri;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                nce of Shigella flexneri 2a: insights into rison with genomes of Escherichia coli K12 Res. 30:4432-4441(2002).
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, Yang G., Wu
J., Kan B.,
D., Qiang B.
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Wu H., Qu D., Dong J
B., Ding K., Chen S.,
g B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       databases
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Best Local
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                                                                                                                                                                                                                                                                             RPOB_SALTY STANDARD; PRT; 1342 AA P06173; Q9L9J8; 01-JAN 1988 (Rel. 06, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update DNA-directed RNA polymerase beta chain (EC beta chain) (RNA polymerase beta subunit). RPOB OR STM4153 OR STMF1.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; 09KWU7; 1HOM.
SWISS-2DPAGE; PO0575; COLI.
ECOZDBASE; D157.0; 6TH EDITION.
ECOGENE; EG10894; rpoB.
InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria;
Enterobacteriaceae; Salmor
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                                                                 Sverdlov E.D., Lisitsyn N.A., Guryev S.O., "Nucleotide sequence of the rpoB gene of s. for the beta-subunit of RNA polymerase.";
Dokl. Biochem. 287:62-65(1986).
                          SEQUENCE
                                                                                                                                                      SEQUENCE FROM N.A.
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GEL; AE000472; AASH8647.1; -.
GEL; M76222; AASH8647.1; -.
GEL; AE016770; AAN83372.1; ALT_INIT.
GEL; AE005630; AAG59183.1; -.
GEL; AE005630; AAG459.1; -.
GEL; W00341; CAA23629.1; -.
GEL; M38292; AAA24579.1; -.
GEL; M38292; AAA24580.1; -.
GEL; M38293; AAA24580.1; -.
GEL; M38287; AAA24581.1; -.
GEL; M38293; AAA24581.1; -.
GEL; M38303; AAA24581.1; -.
GEL; M38303; AAA24581.1; -.
GEL; M38303; AAA24581.1; -.
GEL; M38293; AAA24581.1; -.
GEL; M38303; AA
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SUBUNIT: THE
ENZYME WHICH
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58.3%;
                                                                                                                                                                                                                                         Gammaproteobacteria;
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                                                                                                         ., Monastyrskaya G.S.;
Samonella typhimurium
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Best Local
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Interpro; IPR001572; RNA_pol_B.
Pfam; pF04563; RNA_pol_Rpb2_1; 1
Pfam; pF04561; RNA_pol_Rpb2_2; 1
Pfam; pF04555; RNA_pol_Rpb2_3; 1
Pfam; pF004561; RNA_pol_Rpb2_5; 1
Pfam; pF004560; RNA_pol_Rpb2_7; 1
Pfam; pF04560; RNA_pol_Rpb2_7; 1
                                                                                                                         COMPLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primary scructure gene rpob.";
typhimurium gene rpob.";
Bioorg, Khim, 12:699-707(1986).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
--- TO THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 187-1144 FROM N.A.
MEDLINE-86269165; PubMed-3019156;
Sverdlov E.D., Lisitsyn N.A., Guryev S.O., Smirnov Y.V.,
Rostapshov V.M., Monastyrskaya G.S.;
"Genes encoding the beta-subunit of bacterial RNA-polymerases.
Primary structure of the EcoRI-C fragment of the Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Le Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                       EMBL; X04642; CAA28302.1; --
EMBL; AF170176; AAF23499.1; --
EMBL; AE008894; AAL22981.1; --
EMBL; M38311; AAA27215.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>;</del>
                                                                                                             SEQUENCE
                                                                                                                                                                   Transferase;
                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence LT2 ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lisitsyn N.A., Monastyrskaya G.S., Sverdlov E. "Genes coding for RNA polymerase beta subunit Structure/function analysis.";
Eur. J. Biochem. 177::363-369(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lisitsyn N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: THE ENZYME CONSISTS ENZYME WHICH IS COMPOSED OF ; BETA' CHAIN.
SIMILARITY: Belongs to the R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBSTRATES
CATALYTIC 1
                                                                                                                                                                                                                                                                                            S01794; RNEBBT.
440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [RNA](N).
                          N
                                                     Similarity 7; Conser
                                                                                                                                                                                 PS01166; RNA_POL_BETA;
                                                                                                                                                   proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF.
GEVDDIDHLGNR
                           GEIDIIETIGNR
                                                                                                           401
542
1342
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                                                       Conservative
                                                                                                                                                                   Transcription;
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542
; 150600
                                                                   62.5%;
58.3%;
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                                                    Score 40; DB Pred. No. 48; 3; Mismatches
                                                                                                                                                                   DNA-directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA polymerase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S OF THE SIGMA CHAIN AND THE CO. 2 ALPHA CHAINS, 1 BETA CHAIN,
                                                                                                          > A (IN REF. 4).
> L (IN REF. 1, 2
8143964BF1709C02
                                                                DB
48;
                                                                                                                                                                RNA polymerase;
                                                                                1;
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                                                                                Length 1342;
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                                                                                                           AND 4)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
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Du S., Layman D.,
Mulvaney E.,
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RESULT 11
RPOB_VIBCH
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                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                        InterPro; IPR001572; RNA_pol_B.
Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04561; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF00562; RNA_pol_Rpb2_6; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Googhagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPOB_HAEIN STANDARD; PRT; 1343 AA. P43738; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) DNA-directed RNA polymerase beta chain (EC 2.7.7.6) beta chain) (RNA polymerase beta subunit). RPOB OR HI0515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                           Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                    TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
Pasteurellaceae; Haemophil
NCBI_TaxID=727;
[1]
                                                                                                                                                                                                                                                                                                                                                             EMBL; U32733; AAC22173.1; -. PIR; H64073; H64073.
                                                                                                                                                                                                                                                                                                                                                                                                                                             mod1fied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collabora ween the Swiss Institute of Bioinformatics and the EMBL outstat: Buropean Bioinformatics Institute. There are no restrictions on by non-profit institutions as long as its content is in no by non-profit institutions as long as its content is in no iffed and this statement is not removed. Usage by and for commentation and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RNA)(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                           440
                                                                                                                                                                                                                                                                                                                                  Q9KWU7; 1HQM.
HI0515; -.
                                                                                                                     Similarity 7; Conser
                                                                                      GEIDIIETIGNR
                                                                                                                                                                                             proteome
                                                           GEVDDIDHLGNR 451
                                                                                                                                                                                1343 AA;
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                                                                                                                                   62.5%;
58.3%;
                                                                                                                                                                                149783
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                                                                                                                   <u>ب</u>
                                                                                                                                 Score 40;
Pred. No.
                                                                                                                  Pred. No. 48;
3; Mismatches
                                                                                                                                                                               4EF99CD648686A44 CRC64;
                                                                                                                              DB
48;
                                                                                                                   ?
                                                                                                                                                 Length 1343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
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RESULT 12
RPOB_NEIMA
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Best Local S
Matches 7
RPOB_NEIMA STANDARD;
P57009;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001572; RNA_pol_B.
Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04565; RNA_pol_Rpb2_2; 1.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF04562; RNA_pol_Rpb2_7; 1.
Pfam; PF04560; RNA_pol_Rpb2_7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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Q9KV30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000).

-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES (By Similarity).

-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-El Tor N16961 / Serotype 01;
MEDLINB-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Welson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 1375 AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Transcription; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ptam; PF04560; RNA_pol_Rpb2_7; PROSITE; PS01166; RNA_POL_BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; VC0328; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE004121; AAF93501.1; -. PIR; F82336; F82336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salzberg S.L., Fraser C.M.;
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta chain) (RNA polymerase RPOB OR VC0328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA](N).

SUBGUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND BETA' CHAIN (By similarity).

SIMILARITY: Belongs to the RNA polymerase beta chain family.
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                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 153285 MW;
                                                                                                                                                                                                                                                                                                                                                          62.5%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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RESULT 13
RPOB_N
RPOB_N
ID RPOB_N
AC Q59672
DT 16-OCT
DT 16-OCT
DE DNA-d1
DE beta c
GN RPOB o
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Best Local S
Matches 7
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InterPro; IPR001572; RNA_pol_B.
Pfam; PF04563; RNA_pol_Rpb2_1; 1.
Pfam; PF04561; RNA_pol_Rpb2_2; 2.
Pfam; PF04565; RNA_pol_Rpb2_3; 1.
Pfam; PF00562; RNA_pol_Rpb2_6; 1.
Pfam; PF04566; RNA_pol_Rpb2_7; 1.
Pfam; PF04566; RNA_pol_Rpb2_7; 1.
Pfam; PF04566; RNA_pol_Rpb2_7; 1.
PROSITE; PS01166; RNA_POL_BETA; 1.
                                                       RPOB_NEIMB
Q59622;
01-NOV-1997
16-OCT-2001
16-OCT-2001
        01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.
beta chain) (RNA polymerase beta subunit).
RPOB OR NMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Ratharford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-directed RNA beta chain) (RNA RPOB OR NMA0142.
                                                                                                                                                                                                                                                                                                                                                        Transferase; Transcription; \mathtt{DNA}\text{-}\mathtt{directed} RNA polymerase; \mathtt{Complete} proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Z2491 / Serogroup A / Serotype MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (serogroup A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNA)(N).

SUBUNIT: THE ENZYME CONSISTS O
ENZYME WHICH IS COMPOSED OF 2
BETA' CHAIN.

SIMILARITY: Belongs to the RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AL162752; CAB83457.1;
D82007; D82007.
; Q9KWU7; 1HQM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                            467
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                                                                                                                                                                                                                                                                          7; Conserv
                                                                                                                                                                                                            GEVDDIDHLGNR
                                                                                                                                                                                                                                     GEIDIIETIGNR
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                             A.
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation update)
e beta chain (EC 2.7.7.6) (Transcriptase
e beta subunit).
                                                                                                                                                                                                                                                                        Score 40; DB Pred. No. 50; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF THE SIGMA CHAIN AND THE CO
2 ALPHA CHAINS, 1 BETA CHAIN,
                                                                                                                                                                                                                                                                                                                                        BA4AF438619CB82C CRC64;
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                                      2.7.7.6) (Transcriptase
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CONFLICT CONFLICT

A ->

N REF. 1). N (IN REF. 1). N REF. 1).

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284 350 378 648 648 706 717 748 818 818 819 1190 1201 1244

284 360 378 648 706 718 719 749 818 837 1192 1201 1373

VP -> SA (IN REF. 1).
GG -> A (IN REF. 1).
F -> L (IN REF. 1).
GY -> VN (IN REF. 1).
YNG -> SR (IN REF. 1).

VN (IN REF. 1) SR (IN REF. 1).

MISSING (IN REF. 1) A -> G (IN REF. 1). A -> P (IN REF. 1).

CONFLICT CONFLICT

L -> I (IN KEr. 1).
ILDIFYDKETFYLSSNGVQTDLVADRLKG
ILDIFYDKETFYLSSNGVQTDLVADRLKG N -> L (IN REF. 1).
AYISHTLRTDE -> VISPIPCVRMK (IN RNVLFVFKRCSNRFGRRPSES N -> L (IN REF. 1).

-> NLGYFLRQ
1).

REF.

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Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B. Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E. Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B s
                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentities requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 287:1809-1815(2000).
-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=MC58 / Serogroup MEDLINE=20175755; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nolte O.J.;
Submitted (OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BNCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBSTRATES.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate (RNA)(N).

(RNA)(N).

SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORRESTME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN. AND BETA CHAIN. AND BETA CHAIN. AND BETA CHAIN. AND BETA CHAIN.
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/ Serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10710307;
ders N.J., Heidelberg
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                                                                                                                                                                                                                         DNA-directed RNA polymerase;
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RESULT 14

NIB NYEAST

ID NIPATH

AC P52593

DT 01-0CT

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DE NUCLEO
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RN SEQUEN

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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 110, 120, 120, 130, MEDLINE-96095775; PubMed-8522578;
Altchison J.D., Rout M.P., Marelli M., Blobel G., Wozniak R.W.;
"Two novel related yeast nucleoporins Nup170p and Nup157p:
complementation with the vertebrate homologue Nup155p and functional complementation with the vertebrate pore-membrane protein Pom152p.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Jagels K., Lye G., Moule S., Odell C., Pearson D., Raja Rice P., Skelton J., Walsh S., Whitehead S., Barrell B. "The nucleotide sequence of Saccharomyces cerevisiae ch
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                          interactions with the yeast nuclear pore-membrane prote J. Cell Biol. 131:1133-1148(1995).

FUNCTION: INTERACTS WITH THE CORE STRUCTURE OF THE COMPLEX (NPC). MAY PROVIDE THE NECESSARY ASYMMETRY ANCHORING STRUCTURES SUCH AS CYTOPLASMIC FILAMENTS.

NUCLEDPLASMIC CAGE.

I. SUBUNIT: INTERACTS WITH NUP170 AND/OR POM152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Nucleoporin NUP188 (Nuclear pore protein NU
NUP188 OR YML103C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1187-1205 AND 1611-1629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9169872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288c
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Nehrbass U., Rout
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
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  S47446; S47446.

S0004571; NUP188.

GO:0005643; C:nuclear

GO:0006999; P:nuclear
                                                                                                 X90580; CAA62208.1;
U47107; AAA88904.1;
X80835; CAA56794.1;
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1 (JAN-1996)
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3B-1996) to
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58.3%;
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  pore; IDA.
pore organization
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e EMBL/GenBank
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Pred. No.
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k/DDBJ
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and biogenesis;
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RESULT 15
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GUB_RHOMR
GUB_RHOMR
91-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-raincanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4)
1--allicanase precursor (EC 3.2.1.73) (Lichenase).
                                                                                                                                                                                    ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spilliaert R., Hreggvidsson G.O., Kristjan Eggertsson G., Palsdottir A.; "Cloning and sequencing of a Rhodothermus for a thermostable beta-glucanase and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=21 / ITI-378;
MEDLINE=95010084; PubMed=7925416;
                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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Bacteria; Bacteroidetes; Sphingobacteria; Sph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
MISCELLANEOUS: The enzyme has a temperature optimum of 85 degree: Celsius and a pH optimum of 7.0.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biochem. 224:923-930(1994).
FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN
BUT NOT ON CMC CELLULOSE OR XYLAN.
       156
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TE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                            Similarity 7; Conser
NGEIDIMEHVG 166
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8; Conserv
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63.6%;
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                                                                                                               Score 39;
Pred. No.
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                                                                                                                                                                            BETA-CLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY);
7215C33624135191 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
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                                                                                                                 16;
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Search completed: September 16, 2003, 11:26:28 Job time: 1.91688 secs

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Perfect score:
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 of hits satisfying chosen parameters:
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64
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sp_phage:*
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sp_bacteria:*
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   09c236 neurospora
02660 strongyloce
09ab54 caulobacter
09ewr5 streptomyce
068641 oerskovia x
08gcz7 lysobacter
096tu5 alternaria
                                                                                                             Q95vy3 lumbricus t
077072 eisenia foe
Q51333 oerskovia y
Q9u0g4 pacifastacu
                                                                      Q8n0n3 penaeus mon
Q8mvs9 litopenaeus
O07242 mycobacteri
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ID Q95VY
AC Q95V
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OC Eukaa
OC Lumb
OC Eukaa
OC Humb
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RP SEQU
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Matches 13
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45	44	43	42	41	40	9	38	37	36	35	34	33	32	3	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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# ALIGNMENTS

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RESULT
077072
ID 07
AC 07
DT 01
O77072 PRELIMINARY; PRT; O77072; O1-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Beschin A., De Baetselier P., Bilej M.;

Beschin A. De Baetselier P., Bilej M.;

"Distinct carbohydrate recognition domains of an earthworm defense molecule recognize Gram negative and Gram positive bacteria.";

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

SMBL; AF395805; AAL09587:1; -.

InterPro; IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DUN-2002 (TrEMBLrel. 21, Last sequence update)
01-DUN-2002 (TrEMBLrel. 21, Last sequence update)
Coelomic cytolytic factor precursor.
Lumbricus terrestris (Common earthworm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lumbricina; Lumbricidae; Lumbricus.
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                    SGEIDIIETIGNR 190
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                                                                                                                                                                                                                                                                                                                         382 AA;
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; 5256CF171EB7D3FB CRC64;
                                                                                                                                                                                                                                  Score 64; DB 5;
Pred. No. 0.0023;
Mismatches 0
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                                                                                                                                                                                                                                  Gaps
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RY SEQUENCE FROM N.A.

SPOUTENCE FROM N.A.

REPLINE-98406152; PubMed-9733802;

RA Beschin A., Bilej M., Hanssens F., Raymakers J., Van Dyck E.,

RA Revets H., Brys L., Gomez J., De Baetseller P., Timmermans M.;

RT "Identification and cloning of a glucan- and Lipopolysaccharide-

RT binding protein from Eisenia foetida earthworm involved in the

RT activation of prophenoloxidase cascade.";

RL J. Biol. Chem. 273:24948-24954(1998).

DR EMBL; AF030028; AA035887.; -

DR InterPro; IPR000757; Glyco_hydro_16.

DR Pfam; PF00722; Glyco_hydro_16; 1.

"C SCHIENCE 384 AA; 44322 MW; C90B5C94003BAD6D CRC64;

"C SCHIENCE 384 AA; 44322 MW; C90B5C94003BAD6D CRC64;
RESULT 4
Q9U0G4
ID Q9U0
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Q51333;
Q1-NOV-1996 (
                                                                                                                                                                    J. Bacteriol. 178:4751-4757(1996).

EMBL; U56935; AAC44371.1; -.

HSSP; P23904; IAUK.

InterPro; IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.

SEQUENCE 306 AA; 32835 MW; CD8DB8C1A6
                                                                                                                                                                                                                                                               MEDLINE-96345651; PubMed-8755914; Ferrer P., Halkler T., Hedegaard L., Savva D., Diers I., Asenjo J.A.; "Nucleotide sequence of a beta-1,3-glucanase isoenzyme IIa gene of oerskovia xanthineolytica LL G109 (Cellulomonas cellulans) and initial characterization of the recombinant enzyme expressed in Bacillus subtilis.";
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     Q900G4
                                                                                                                                                                                                                                                                                                                                                                                  Micrococcineae;
NCBI_TaxID=1710;
                                                                                                                                                                                                                                                                                                                                                                                           Oerskovia xanthineolytica.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Promicromonosporaceae; Cellulosimicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-OCT-2002
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Lumbricina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eisenia foetida (Common brandling worm) (Common dung-worm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
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01-OCT-2001 (TrEMBI
Coelomic cytolytic
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NCBI_TaxID=6396;
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                                                                                                                       Similarity
9; Conserv
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                                                                                          SGEIDIIETIGN 12
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     PRELIMINARY;
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75.0%;
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Last annotation update)
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Pred. No.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation updat
''nonolvsaccharide and beta-1,3-glucan binding pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative secreted protein.
Aedes aegypti (Yellowfever mosquito).
Eukaryota, Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purification, characterization, and cDNA cloning.";
J. Biol. Chem. 275:1337-1343(2000).
EMBL; AJZ50128; CAB65353.1;
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
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Lee S., Wang R., Soderhall K.;
"A lipopolysaccharide- and beta-1,3-glucan-binding protein from hemocytes of the freshwater crayfish Pacifastacus leniusculu:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Black eye; TISS Valenzuela J.G., Pham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2002 (TrEMBLrel. 22, 01-oCT-2002 (TrEMBLrel. 21, 01-oCT-2002 (TrEMBLrel. 22, 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pacifastacus leniusculus (Signal crayfish).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malaco
Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Astacoidea; Astacidae; Pacifastacus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8T9V2
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SGEVDLMESRGNR
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16
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Pham V.M., Garfield M.K.,
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361
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75.0%;
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Pred. No. 3.1;
4; Mismatches
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Pred. No.
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; 93A5E67911ED6619 CRC64;
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3.1;
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era; Culicoidea; Aed
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                                                                                                                                                                                        Length 371;
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                                                                                                                                                                                                                                                          CRC64;
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Submitted (APR-2001) to the EMBL/GenBa:
EMBL; AF368168; AAM21213.1;
Interpro; IPR000757; Glyco_hydro_16; 1.
SEQUENCE 366 AA; 41497 MW; 6F540A6
  007242
007242;
01-JUL-1997
01-JUL-1997
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OBNON3;
OBNON3;
O1-OCT-2002 (TrEMBLrel. 2
O1-OCT-2002 (TrEMBLrel. 2
O1-MAR-2003 (TrEMBLrel. 2
D1-MAR-2003 (TrEMBLrel. 2
Beta-1,3-91ucan binding penaeus monodon (Penoeid
                                                                                                                                                                                                                                                  TISSUE-Hepatopancreas;
TISSUE-Hepatopancreas;
MEDLINE-22068042; PubMed-12072514;
Roux M.M., Pain A., Klimpel K.R., Dhar A.K.;
The Lipopolysaccharide and beta-1,3-Glucan Binding Protein
"The Lipopolysaccharide and beta-1,decided Shrimp (Pengeus
                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Lipopolysaccharide and beta-1,3-glucan binding protein.
Litopenaeus styllrostris (blue shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Perenaidae; Litopenaeus.
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Penaeus monodon (Penoeid shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea;
Eumalacostraca; Eucarida; Decapoda; Dendrok
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Pro; IPR000757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
NCE 376 AA; 42610 MW; D7ADC
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  (TrEMBLrel.
                                                                                                                                          Conservative
                                     PRELIMINARY;
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                                                                                                                                                   71.9%;
75.0%;
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75.0%;
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2; Mismatches
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Last sequence update)
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Pred. No. 4.7;
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D7ADC5A310208885 CRC64;
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6F540A60E83FDD7D CRC64;
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TUDETCULLIST; RV0315; --
TUDETCULLIST; RV03757; G
InterPro; IPR000531; 7
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01-JUN-2001
01-OCT-2001
                               SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
                                                                                                                Neurospora crassa.
Eukaryota; Fung1; Ascomycota;
Sordariales; Sordariaceae; Neu
NCBI_TaxID=5141;
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CONFLICT
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                            B7A16.110.
                                                                                                                                                                                                                                Related
                                                                                                                                                                                                                                                                                                                      Q9C236;
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InterPro; IPR006311; Tat.
Pfam; PF00722; Glyco_hydro_16; 1.
TIGRPAMS; TIGR01409; TAT_signal_seq; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2001) to the EMBL; Z96800; CAB09586.1; -EMBL; AE006940; AAK44553.1;
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Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva
Delcher A., Utterback T., Weldman J., Khouri H., (
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Corynebacterineae; Mycobacteriaceae;
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        isel J., Brandt P., I
Mannhaupt G.;
he EMBL/GenBank/DDBJ
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5.6;
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M., Haft D., Hickey E.,
Ermolaeva M., Salzberg
ouri H., Gill J., Mikul
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SEQUENCE FROM N.A.

German Neurospora genome project;

German Neurospora genome project;

Submitted (FEB-2001) to the EMBL/GenBa

EMBL; AL513445; CAC28724.1; -.

InterPro; IPR000757; Glyco_hydro_16.

Pfam; PF00722; Glyco_hydro_16; 1.

SEQUENCE 462 AA; 51868 MW; 28808B6
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01-NOV-1996 (TremBLr
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Beta 1,3-glucanase
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Q9AB54;
01-JUN-2001
01-JUN-2001
01-MAR-2002
     STRAIN-ATCC 19089 / CB15;

MEDLINE-21173698; PubMed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., E

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Wh
                                                                                                                      Caulobacter crescentus.
Bacteria; Proteobacteria; Alph
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
                                                                                                                                                                    Beta-glucanase.
CC0380.
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Q26660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinocea; Echinoide; Strongylocentrotidae;
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MEDLINE=96270625; PubMed=8692900;

Bachman E.S., McClay D.R.;

"Molecular cloning of the first metazoan beta-1,3;

"Molecular cloning trongylocentrotus purpuratus.";

Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

EMBL: U49711; AAC47235.1;
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NCBI_TaxID=7668;
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                                            EMBL;
HSSP;
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Nature 417:141-147(2002).
EMBL; AL939106; CAC14352.1;
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MEDLINE-21996410; PubMed=12000953;
MEDLINE-21996410; PubMed=12000953;
Mentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil
                                                                                                            Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Ta; Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhil
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF00652; Ricin_B_lectin; 3.
                                                                                      "Complete genome
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MEDLINE=97000351; PubMed=8843436;
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Cerdeno A.M.,
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01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                           Redenbach M.,
                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomycineae;
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Pfam; PF00722; Glyco_hydro_16; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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Streptomyces coelicolor
robiol. 21:77-96(1996).
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O'Neil S
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Best Local Similarity
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Best Local
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InterPro; IPR000757; Glyco_hydro_16.

InterPro; IPR000772; Ricin_B_lectin.

Pfam; PF00722; Glyco_hydro_16; 1.

Pfam; PF00652; Ricin_B_lectin; 3.

SMART; SM00458; RICIN; 1.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.

PROSITE; PS50231; RICIN_B_LECTIN; 1.
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068641;
                                                                                                                                                                                                                                                                                                                           rerrer P., Andrews B.A., Asenjo J.A., Hedegaard L., Diers I.;
"BglII codes for a yeast-lytic beta-1,3-glucanase from Oerskovia
xanthineolytica LL G109 (Cellulomonas cellulans) having a mannoss
binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-96250169; PubMed-8659924;
Ferrer P., Hedegaard L., Halkier T., Diers I., Sa "Molecular cloning of a lytic beta-1,3-glucanase xanthineolytica LL G109.";
Ann. N. Y. Acad. Sci. 782:555-566(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oerskovia xanthineolytica.
Bacteria; Actinobacteria; Actinobacteri
Micrococcineae; Promicromonosporaceae;
                                                                                                                                                                                                                                                                               Submitted (MAR-1998) to the EMBL; AF052745; AAC38290.1;
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PROSITE; PSO1034; GLYCOSYL_HYDROL_F16; PROSITE; PS50231; RICIN_B_LECTIN; 1.

Hydrolase; Complete proteome.

SEQUENCE 422 AA; 44143 MW; 71050471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular characterisation of a thermoactive 
Oerskovia xanthineolytica.";
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Asenjo J.A., Dobson C.M.;
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68.8%;
72.7%;
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Score 44;
Pred. No.
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Alternaria alternata.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
NCBI_TaxID=5599;
                                                                              NON_TER
SEQUENCE
                                                                                                          Eshel D., Prusky D., Dinoor A.;
"Mixed-linked glucanase precursor of Alternaria alternatic Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF283319; AAK69516.1; -
InterPro; IPR000757; Glyco_hydro_16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
                                                                                                                                                                                                                                       Q96TU5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 2), Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palumbo J.D., Sullivan R.F., Kobayashi D.Y.; "Molecular characterization of three beta-1,3-glucanase ge Lysobacter enzymogenes strain N4-7 and partial biochemical characterization of their gene products by expression in
                                                                                                                                                                                                                                                                                       Q96TU5
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Bacteria; Proteobacteria;
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Oerskovia xanthine
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Bombyx mori mature
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## ALIGNMENTS

RESULT 1 AAY24914

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       Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical.
                                   Drosophila melanogaster polypeptide SEQ ID NO 15111.
                                                                  26-MAR-2002
                                                                                             ABB62773;
                                                                                                                      ABB62773 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection capable of detecting 1000 or more genes from Drosophila. The
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                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL06876
                         NAMOVDYIRVY
                                                                      ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                       -ALKIDYVRVF
                                                                                                         LFSVDGQVYGEMLNGFTELDENP.
                                                                                                                                REFYDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHF
                                                                                                                                                           KLVD----GRSLYGGP-----VLSTDAHQREDLWLSKRKISHFGDDFHTYSLDWSSNRL
                                                                                                                                                                                   EFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDW-----
                                                                                                                                                                                                                TFAFQYGRIEIRAKLPKGDWIVPLLLLEPLTEWYGQSGYESGQLRVALARGNSVLRMPRG
                                                                                                                                                                                                                                 KYSFTHGRVVVHAKMPVGDWLWPAIWMLP-EDWVYGGWPRSGEIDIIETIGNRDFKNTGG
                                                                                                                                                                                                                                                                                            QTGAPEGTDEMYNGVLDVWAMYGACTNTDN--NGCY----RTGAAGDIPPAMSARVRTFQ
                                                                                                                                                                                                                                                                                                                         LLFEETFDQLNESLWIHDVRLPLDSKDAEFVLY--DG-KAKVHDGNLVIEP-LLWSSYRP
                                                     SLGVSVGGFGDF----
                                                                                                                                                                                                                                                                       DLS-----IANSRLD---LSERCTGTHNRIKECILHSTGSGPSGIMPPIVTPRISTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  492 AA;
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO 15111; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                           15.9%;
                          381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PWD,
                                                  ·VDHLRTATYEKPWAN--YHPQAKLQFHQAQDQWLPTWKQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or more genes from Drosophila. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                                                                                           Score 357; DB 22;
Pred. No. 6.8e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                꾶
                                                                                                                                                                                                                                                                                                                                                                               133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        format directly from
                                                                                                                                                                                                                                                                                                                                                                                                      Length 492;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                    -NYGDNFHTFWFDWSPNGL
                                                                                                       RWKQGGPMAPFDKMFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reagent
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alling and
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT

430

340 197

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                                                                                                                                          This sequence comprises the polypeptide precursor of a novel Coerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89157). Claimed DNA constructs that encode the novel BG (see Also AAW29455), a mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal construction of acterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby cended amount of contaminants. They can also be used for the production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to
                                                                        Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                          New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for obtaining desirable products
                                                                                                                                                                                                                                                                                                                                                                           Diers I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-1,3-glucanase; lytic enzyme; yeast; beta glucan degradation; fungal cell wall; intracellular product; purification; protoplast
                                                                                                            Sequence
                                                                                                                                                                                                                                                                                            Example 2; Page 42-43;
                                                                                                                                                                                                                                                                                                                                                                                           (NOVO)
                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-1996;
12-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oerskovia xanthineolytica beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW29457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW29457
                                                                                                                                                                                                                                                                                                                                                         1997-526451/48.
  106
                   81
                                     57
                                                      26
                                                                                                                                     protoplasts
                                                                                                                                                                                                                                                                                                                                                                                           NOVO-NORDISK AS.
                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                 AAT89157
                 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY
                                              LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                          Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xanthineolytica LLG109 (DSM 10297).
                                                                                                            303
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                           96DK-0000885
96DK-0000427
                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=
53..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                               15.6%;
                                                                                                                                                                                                                                                                                                                                                                           Halkier
                                                                                                                                                                                                                                                                                         64pp; English.
                                                                                                                                    use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sig_peptide
                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303
                                                                      Score 350; DB 18;
Pred. No. 1.6e-24;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                           Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                          Hedegaard

    obtained from Oerskovia
the lysis of microbial cells

                                                                                       Length 303;
                                                                       Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protoplast
--TSARMTTQGKY
                                                                       Gaps
                 140
                                                     80
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RESULT 4
AAW29456
ID · AAW2
                                New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for obtaining desirable products
                                                                                                                                                           Diers
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12-APR-1996;
                                                                                                                                                                                                                                                                                  14-APR-1997;
                                                                                                                                                                                                                                                                                                                                                        WO9739114-A1
                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oerskovia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-1,3-glucanase; lytic enzyme; yeast;
fungal cell wall; intracellular product;
Example 2; Page 39-40; 64pp; English.
                                                                                                                                                                                            (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                     23-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oerskovia xanthineolytica beta-1,3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW29456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29456 standard;
                                                                                                      1997-526451/48.
DB; AAT89156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
:||:' ::| | :|| ||| ||| :| :| :| :| :| :| :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHRVTRASVGANAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPQYGRIEARIQIPRGQGIWPAFWMLGGSFPGTPWPSSGEIDIMENVGFEPHRVHG----
                                                                                                                                                         Ferrer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xanthineolytica LLG109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
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                                                                                                                                                                                                                             96DK-0000885
96DK-0000427
                                                                                                                                                                                                                                                                                  97WO-DK00160
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
53..435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TVH-GPGYSGGS-GITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVD--GQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /label= Mannose-binding_domain
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                           Halkier
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435
                                                                                                                                                           Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DSM
                                                                                                                                                           Hedegaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10297).
                                                   the
                                               obtained from Oerskovia
ne lysis of microbial cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta glucan degradation; purification; protoplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VFDQPFFLILNVAVGGQW
                                                     microbial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protoplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QQMKVDYVRV
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This sequence comprises the polypeptide precursor of a novel Oerskovia xanthineolytica enzyme that exhibits beta-1,3-glucanase (BG) activity and which includes a mannose binding domain (MBD). Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89156). Claimed DNA constructs that encode the novel BG lacking a MBD (see AAW29455 and AAW29457), a MDB (see

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ARESULT 5
AAW29457
ID AAW2
XX
AC AAW2
XX
DT 14-A
DT 14-A
DT 14-A
CO OOTS
XX
Beta
KW Bung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG polypeptides, with or without a mannose binding domain, in fung or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to prepare protoplasts for use in fusion, transformation and cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW29458),
BG polypept
                                                                  mat_peptide
                                                                                                                                                                0erskovia
                                                                                                                                                                                                                                 Oerskovia xanthineolytica mature beta-1,3-glucanase
                                                                                                                                                                                                                                                             14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
  23-OCT-1997.
                                                                                             sig_peptide
                                                                                                                                                                                                         Beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                  AAW29455 standard; Protein;
                            WO9739114-A1
                                                                                                                                                                                           fungal cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                              381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                         PGYPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHRVTRASVGANAW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPQYGRIEARIQIPRGQGIWPAFWMLGGSFPGTPWPSSGEIDIMENVGFEPHRVHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ------
                                                                                                                                                                xanthineolytica LLG109
                                                                                                                                                                                                                                                                                                                                                                                                              381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or the full-length enzyme can be used to produce recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                  /*tag= }
164..952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TVH-GPGYSGGS-GITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVD--GQQ
                                                       /*tag=
                                                                                             23..120
                                                                                                                                   Location/Qualifiers
                                                                                                          /*tag=
                                                                                                                                                                                       e; lytic enzyme; yeast;
intracellular product;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TTQLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%;
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Pred. No. 2.6e
30; Mismatches
                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                              MSG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18;
.6e-24;
                                                                                                                                                                                        purification;
                                                                                                                                                                                                        beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                      glucan degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme that exhibits beta-1,3-glucanase (BG) activity. Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT89155). Claimed DNA constructs that encode the novel BG also AAW29456 for corrected sequence), a mannose binding domain (see AAW29456), can be used to produce recombinant BG polypeptides, with or without a mannose binding domain, in fungal or bacterial host cells. BG polypeptides are used for the degradation or modification of beta-glucan containing material, especially for the gentle lysis of microbial cell walls, thereby enabling recovery of desirable intracellular products with a reduced amount of contaminants. They can also be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of e.g. pigments, colourants, flavourants, yeast extracts, pharmaceuticals, food or feed compositions, and to prepare protoplasts for use in fusion, transformation and compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated beta-1,3-glucanase enzyme xanthineolytica, used particularly for obtaining desirable products
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide comprises a novel Oerskovia xanthineolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 35-36; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1996;
12-APR-1996;
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237 Y
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                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                     NINPOTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrer
                                                                                                                                                                                  GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
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                                                     PGYPDG-
                                                                            GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV
                                                                                                        FHRVTRASVGANAW
                                                                                                                                                                                                                    QPQYGRIEARIQIPRGQGIWPAFWMLGGSFPGTPWP-SGEIDIMENVGFEPHRVHG----
                                                                                                                                                                                                                                                                                                                                LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ------
                                                                                                                                  LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN
                                                                                                                                                               ----TVH-GPGYSGGS-GITGMYQHPQGWSFADTFHTFAVDWKPGEITWFVD--GQQ
237
                         381
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96DK-0000427
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Pred. No. 1.1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transformation and cloning
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ne lysis of microbial cells
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18;
                                                                                                                                                                                                                                                                                                                                                                                       95;
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RESULT 6

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AAR89136
IID AAR8
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Best Local S
Matches 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic shock, a encoding it, for producing transgenic plant(s) resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacter cloacae;
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                                                                                                                                                                                         188
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                                                                                                                                                                                                                                                                                                                                                                                                101;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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GGEFLGIQKMGSTMHWGPGWD-DNRYWLISLPKHSDDWNYGDNFHTFWEDWSPNGLRFFV : | ::||:||: | :: |
                                                                                                            HGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWP-RSGEIDIIETIGN-----RDFKNT
                                                                                                                                                                                                                            TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT
                                                                                                                                                                                                                                                                                                                                 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ
                                                                          YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                 QHMPGFLDDSIYSGTLN---LFSGCTSS-AEACIKQASGADILPPIVSGRI-TSIGFAFT
                                                                                                                                                                                                                                                                                 IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI:-----NAKLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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27.3%;
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58; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 314; DB 17;
Pred. No. 6.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                        68;
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RESULT 7
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                                                                                                               Claim 5;
                                                                                                                                   attack
                                                                                                                                         New protein from Bombyx mori that binds bacterial lipopoly-saccharide - esp. used to treat septic shock, also DNA encoding it, for producing transgenic plant(s) resistant to fung
                                                                                                                                                                                          WPI; 1996-060094/07
                                                                                                                                                                                                            Brey PT,
                                                                                                                                                                                                                                                   09-JUN-1994;
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                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                          FR2721032-A1
                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                          tobacco;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR89137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 lipopolysaccharide binding protein; Bombyx mori; haemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397
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                                                                                                                                                                                 AAT10279
                                                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                             Lee
                                                                                                                                                                                                                                                                                                                                                                                                                          tomato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SLIVDFVKV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAMOVDYIRV 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGITEF-RDGSITSGG----VTKPW-----RDSARKASVHFWRHMSDWFPRWSQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGEEWARVEAPRDAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                               42-43;
                                                                                                                                                                                                                                                                    94FR-0007083.
                                                                                                                                                                                                                                                                                                                                       /note=
182
                                                                                                                                                                                                                                                                                                                                                        /note=
13..467
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        potato; fungal infection; fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VLYGGPIMDLECRENFLSTKRRRDGTSWGDSFHTYSVQWTPDFIALSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                            53pp;
                                                                                                                                                                                                                                                                                                                           "putative N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                 "signal
                                                                                                                                                                                                                                                                                                                                              "mature protein"
                                                                                                               French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467
                                                                                                                                                                                                                                                                                                                                                                peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAVCAHAPRHLLQAGSQMAPFDDHFYITLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                 ph; primer;
lification;
lant; vine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443
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This is the amino acid sequence of the full length lipopolysaccharide (LPS) binding protein from Bombyx mori. The protein was isolated from the haemolymph of fifth stage B.mori larvae after injection with Enterobacter cloacae strain 57-9. Partial amino acid sequence was used to generate PCR primers (AAT10280-1). These amplified a fragment of the gene used as a probe to obtain the full length gene by screening a CDNA library derived from B.mori previously injected with heat-killed E.cloacae. The protein or fragments of it, can be used to treat diseases associated with LPS complexes e.g. septic shock, to remove LPS from

products used for

injection and to protect transgenic plants r potato, against fungal infections.

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
The new enzyme is derived from alkaoplhilic Bacillus Sp. The enzyme acts on beta-1,3-glucans to form glucose and laminaribiose. It is stable over a wide pH range with opt. activity at weakly actidic pH and has good heat resistance.
                                              Claim 7; Fig 2; llpp; Japanese
                                                                 Heat resistant beta-1,3-glucanase alkali-compatible Bacillus sp.
                                                                                              WPI; 1991-113290/16.
N-PSDB; AAQ11293.
                                                                                                                                              20-JUL-1989;
                                                                                                                                                               20-JUL-1989;
                                                                                                                                                                                  07-MAR-1991
                                                                                                                                                                                                     JP03053883-A.
                                                                                                                                                                                                                       Bacillus sp
                                                                                                                                                                                                                                           Alkalophilic;
                                                                                                                                                                                                                                                            Beta-1,3-glucanase
                                                                                                                                                                                                                                                                                25-MAR-2003
18-JUN-1991
                                                                                                                                                                                                                                                                                                             AAR11599;
                                                                                                                                                                                                                                                                                                                               AAR11599 standard;
                                                                                                                          (SHKJ ) SHINGIJUTSU
                                                                                                                                                                                                                                                                                                                                                                             456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 VWQDEFDYFDGAKWQ-HEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SLIVDFVKV 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHMPGFLDDSIYSGTLN---LFSGCTSS-AEACIKQASGADILPPIVSGRI-TSIGFAFT
                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGITEF-RDGSITSGG---VTKPW-----RDSARKASVHFWRHMSDWFPRWSQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGEFLGIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGTVEIRAKLPQGDWLYPEILLEPFLKKYGSMNYASGVVKIACARGNAELYSGPNDYSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAP-FGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI-PPAMSARVRTFQKYSFT
                                                                                                                                                                                                                                                                                                                                                                                               NAMOVDYIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK----FFDARGNWKWTWDDEGDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGEEWARVEAPRDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VLYGGPIMDLECRENFLSTKRRRDGTSWGDSFHTYSVQWTPDFIALSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFEEQFDSLDENVWQIEQYIPIYHPEYPFVSYQRNNLTVSTADGNLHI-----NAKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                           heat resistant.
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                                                                                                                                             89JP-0185928
                                                                                                                                                                89JP-0185928
                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                              380
                                                                                                                          KAIHATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                               A
                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAVCAHAPRHLLQAGSQMAPFDDHFYITLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7e-21;
                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
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                                                                            derived
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                                                                            from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314
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RESULT 9
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                           The present sequence is beta-1,3-glucanase from I protein can be used in various industrial fields cake and bread manufacture and brewing.
                                                                                                                                                                                                               Beta-1,3-glucanase and beta-1,3-glucan-binding
                                                                                                                                                                                                                                                                WPI; 2001-364762/38.
N-PSDB; AAH46359, AAH46360.
                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2001120280-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-1,3-glucanase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB99272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB99272 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                Claim 1; Page 8-9; 12pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                             (MEIJ ) MEIJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --MLVDYVRVYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG-----DNFHTFWFDWSPNGLR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSLVWSDEFNGNSLNPANWTAEIGTGSGGWGNNELQYYTSRPQNLQVSGGNLII--TAQR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GTVH-----WDAN------GHAE---YGRTSGNLDFSQYHTYSVEWEPNYIR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSFRYGKIEARIKLPSGQGLWPAFWMLGEDFSSVGWPYCGEIDIMERVNNNPHVN----- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ES-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILNLAVGG---
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                                                                                                                                                                                                                                                                                                                                          SEIKA KAISHA
                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0311073
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0311073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme; stockbreeding; bread
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
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                                                                                                                                                                                                                                                                                                                                               LTD
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Pred. No. 7.8e-21;
5; Mismatches 83;
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                                                                                                                                                                                                               peptide
                                                   Bacillus
s such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    manufacture;
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                                                      circulans. The stockbreeding,
                                                                                                                                                                                                                  their genes
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RESULT 10
AAR97362
ID AAR97
XX AAR97
XX AAR97
XX OGESK
XX Beta-
KW Bytic
KW Bytic
KW Pigme
XX OGESK
XX FH Key
FT Pepti
FT Pepti
FT Pepti
FT Prote
FT Prote
XX W996:
XX W996:
XX AR96
PF 16-O
XX ONOV
XX ASEN
PI ASEN
PI ASEN
PI ASEN
PI SAVV
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                                                                                                                                                                                                                                                                             Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; colorant; flavour; yeast extract; protoplast.
                                                                                                                                                                                                                                                                                                                             Oerskovia beta-1,3-glucanase.
WPI; 1996-222000/22
                      Savva
                               Asenjo JA,
                                                                            14-OCT-1994;
                                                                                                                         25-APR-1996
                                                                                                                                              WO9612013-A1
                                                                                                                                                                               Protein
                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                              Oerskovia
                                                                                                                                                                                                                                                                                                                                                      03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                            AAR97362;
                                                                                                                                                                                                                                                                                                                                                                                                 AAR97362 standard;
                                                                                                 16-OCT-1995;
                                                                                                                                                                                                                           Peptide
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                                                      NOVO ) NOVO-NORDISK
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|||:||:
|VDYVRVYQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDN----FHTFWFDWSPNGLRFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNLVWSDEFNGTSLNRANWTPEIGTGSGGWGNNELQYYTDRAQNVQVTGGNLVI--TAQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMO 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV
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                                                                                                                                                                                                                                                           xanthineolytica strain LLG109 (DSM 10297).
                               Diers I,
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                                                                           94DK-0001192
                                                                                                 95WO-DK00414
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                                                                                                                                                                   /label= Pro_peptide 64..306 /label= Mat_protein
                                                                                                                                                                                                    /label- Sig_peptide 36..63
                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                               Ferrer P,
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                                                                                                                                                                  Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                 306
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Pred. No. 3.1e-20;
7; Mismatches 90;
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                                Halkier
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                              Hedegaard
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27-SEP-2001 WO200171042-A2 Drosophila melanogaster

pharmaceutical Drosophila;

developmental biology; cell signalling; insecticide;

Drosophila melanogaster

polypeptide SEQ

ID NO 10332

26-MAR-2002

(first entry)

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RESULT 11
ABB61180
ID ABB61
XX ABB61
XX ABB61
XX ABB61
XX Drosc
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Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A novel beta-1,3-glucanase (AAR97362) from Oerskovia xanthineolytica LLG109 is useful for degrading or modifying beta-glucan-contg. material. Its amino acid sequence was deduced from a genomic DNA sequence (AAR29043) isolated from an O. xanthineolytica library. Recombinant beta-1,3-glucanase can be produced on a large scale using transformed host cells, esp. Bacillus subtilis DN1885 or ToC46. Protease-free beta-1,3-glucanase can be obtd. that is useful for Lysing fungal cell walls, allowing recovery of intracellular proteins. The enzyme is also useful for the prepn. of protoplasts and for the prodn. of pigments, colorants, flavours, yeast extract
                                                                                                                                                                                                                 ABB61180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA construct encoding enzyme with beta-1,3-glucanase activity - useful for modifying or degrading beta-glucan contg. material and the prepn. of e.g. food colourants, flavourings and yeast extracts
                                                                                                                                                                                                                                                 ABB61180
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and pharmaceuticals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPQFGRIEARIQIPRGQGIWSAFWMVGANLPDTPWPTSGEIDIMENVGNAPHEVHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TVH-GPGYSGDN--GIMGTYQHPQGWSFADDFHNFGIDWTPGEITWLVD--GQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 AA;
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Pred No. 2e-19;
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RESULT 12
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Matches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10151), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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 18-AUG-1998
                    AAW56275;
                                       AAW56275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
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DB; ABL05283.
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                                       standard;
                                                                                                                                     WAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFF
                                                                                                                                                                                                                                                                                                                     LVFVDEFNAAKLDPNKWKAERRFSGQPDYEFNVYVDDAPETLCLANGHVVLSTNTMKKQF
                                                                                     KEVKKIRDHWLDEGH - -
                                                                                                       DARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                          LEEGTGLAPFDQEFYLTFGLSVGGFNEYQHE:
                                                                                                                                                                                   VDDENQALLDVPYPLIDANPWWVDFWEWGKPW-----
                                                                                                                                                                                                       AVLFADEPLRSVKNCLKPGTG-
                                                                                                                                                                                                                        GGEFLG--IQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFF
                                                                                                                                                                                                                                           FSFKYGRVEVRAKMPRAQWVTPQIWLQPRRPIYGVDDYRSGQLRIAYTRPNGGNLDLYGA
                                                                                                                                                                                                                                                             YSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYG-GWPRSGEIDIIETI---GNRDFKNT
                                                                                                                                                                                                                                                                                                 NPQTGAPFGTDFMYNGVLDVWAMYGACTNTDN-NGCYRTGAA--GDIPPAMSARVRTFQK
                                                                                                                                                                                                                                                                                                                                        IVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGANSF-VRDGKLFIKPTLLADNI
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                                                                                                                                                                                                                                                                                                                                                                                                 490 AA;
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                                                                                                                                                                                                                                                                                                                                                           Conservative
 (first entry)
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2000US-0614150
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                                       Protein;
                                                                                                                                                                                                                                                                                -----LDLGE----KCTGQANTHDCVRNGRTLNDGLPPMVTAQFSS-KD
                                                                                                                                                                                                                                                                                                                                                                 13.2%;
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                                                                                      -MKIDYVKVY
                                                                                                                                                                                                                                                                                                                                                           57;
                                        422
                                                                                                                                                                                                                                                                                                                                                         Score 295; DB
Pred. No. 4.6e
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          No. 4.6e-19;
smatches 127;
                                                                                                                                                                                                      -----NNSEDWS--DSFHNYTLEWTPRELRWL
                                                                                                                                                                 -GKEWCVQGSAKGSFSETTAAGKSLPQAQK---
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated endo-beta-galactosidase - from Flavobacterium keratolyticus, used particularly for de-antigenising human erythrocytes bearing Al antigen for blood transfusions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 19
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-N-acetylgalactosaminidase;
erythrocyte; transfusion; blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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DB; AAV22722.
                                                                                                                     173
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  302
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APFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                         TMIWSPNDIRFYV --- NNSL--
                                                                              WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL
                                                                                                                                                            DITETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTF
                                                                                                                                                                                                                        AGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPED-WVYGGWPRSGEI
                                                                                                                                                                                                                                                                                  NLVLR-----
                                                                                                                                                                                                                                                                                                                       NSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGA
                                                                                                                                                                                                                                                                                                                                                              LINATTVATTD---YELIWSDEFNSSGGFDSTKWSYADRGTVAWNKYMTSLPAYASQDGS
                                                                                                                                                                                                                                                                                                                                                                                                 LLFGEGFAFTDWDQYHIVWQDEFDY---FDGAKWQHEVTATGGGN---SEFQLY-TQDGA
                                                                                                                       DSMEHVNNESV--
                                                                                                                                                                                                 AGDPVAYHAGGVKSMGKFSMTYGKVEVRAKFTQGRGSWPAIWMMPEPATAYGGWPSCGEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2A-2B;
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47..422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 286.5; DB 19; 27.0%; Pred. No. 2.4e-18; tive 32; Mismatches 100;
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                                                                                                                       -MYHTIHNGSVTNANG---GSTASKSATYNTTD-YNLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endo-beta-galactosidase;
typing reaction; keratan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lenny
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                                                                                                                                                                                                                                                                                -MDNAVV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or in blood typing
                                       -QYTYARVSGGGTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          147;
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RESULT 13
ABB60444
ID ABB60
XX ABB60
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XX ABB60
XX Drosc
KW Drosc
KW Drosc
KW Pharm
OS Drosc
FM WO200
YX 27-SI
YX 23-MJ
PF 23-MJ
PF 23-MJ
PF 23-MJ
PR 11-JU
PR 11-JU
PR 11-JU
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PR N-PSI
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DR N-PSI
XX WPI;
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                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences (ABL0184)
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter
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pharmaceutical.
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DB; ABL04547.
136 TFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFK-N 194
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                     QYHIVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGA-NSFVRDGKLFIKPTLLA
                                                                                                                                 DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI----PPAMSARVR 135
                                                                                                                                                                                    QGELIFEDNFSEAQLNKTTWKHDIRQRMYHVEEELVAFDDAARNCFVKEGELHIVPTIAT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                    410 AA;
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2000US-0614150.
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24.5%;
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                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                        Score 249.5; DB 2
Pred. No. 6.9e-15;
2; Mismatches 143
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                                                                              -LGDRCTAVESPEQECNIAHGIFYSIKPPVFSAQIH
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                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                           143;
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RESULT 14
ABB60451
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Query Match 11.1%;
Best Local Similarity 24.5%;
Matches 91; Conservative 5
                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG176-ABLIG511).
                                                                         The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                     Sequence
                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB60451 standard;
                                                                                                                                                                                                                                   Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                     New isolated nucleic
                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75
N-PSDB; ABL04554.
                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB60451;
                                                                                                                    (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE
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                                                                                                                                                                                                                                                                    solated nucleic acid from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAMVIDYVRVY 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVGGTNGFIPDGCINRGGDPAL----QKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
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2000US-0614150
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                                                                                                                                                                                                                                   NO 8145;
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                                                                                                                                                                                                                                                                       detection reagent for detecting 1000 or for elucidating cell signalling and cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biology;
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                                                                                                                                                                                                                                 21pp + Sequence Listing;
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Score 249.5; DB Pred. No. 6.9e-152; Mismatches 14
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RESULT 15
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Peptide
AAQ81334 encodes AAR67915 a (1-3)-beta-D-glucan sensitive factor, it has a high affinity for the (1-3)-beta-D-glucan found in fungal
                                Claim 9; Pages 23-32; 51pp; Japanese.
                                                                DNA encoding a polypeptide comprising a tetrapeptide motif at least once - which may be used as an antibacterial and
                                                                                                 WPI; 1995-060996/08.
N-PSDB; AAQ81334.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAR67915;
                                                                                                                                                                            29-JUN-1993;
                                                                                                                                                                                                 29-JUN-1994;
                                                                                                                                                                                                                       12-JAN-1995.
                                                                                                                                                                                                                                           WO9501432-A1
                                                                                                                                                                                                                                                                                                           Limulus sp.
                                                                                                                                                                                                                                                                                                                                mycosis diagnosis.
                                                                                                                                                                                                                                                                                                                                       (1-3)-beta-D-glucan sensitive factor; antifungal agent;
                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR67915 standard; Protein;
                                                                                                                                 Iwanaga S,
                                                                                                                                                      (SEGK ) SEIKAGAKU KOGYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                               (1-3)-beta-D-glucan sensitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAMVIDYVRVY 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVGGTNGFIPDGCINRGGDPAL----QKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRNSFSFKFGKIVVRAKLPKGDWLFPYLMLQPVS-TYAETHYAKQLRIAYARGNANLRTK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-----VTDGSFK-----LGDRCTAVESPEQECNIAHGIFYSIKPPVFSAQIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDI----PPAMSARVR 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYHIVWQDEFD--YFDGAKWQHEVTATGGGNSEFQLYTQDGA-NSFYRDGKLFIKPTLLA
                                                                                                                                 Muta T,
                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                            93JP-0184403
                                                                                                                                                                                                94WO-JP01057
                                                                                                                                                                                                                                                             Location/Qualifiers
1..19
/label= sig_peptide
                                                                                                                                 Oda T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381
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                                                                                                                                Seki N;
                                                                                                                                                                                                                                                                                                                                                                factor.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell walls. The protein is therefore useful for clinically diagnosing mycosis, and as an antifungal agent for the removal of fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
240
                353 FFDARGNWKWTWDDEGDNNAMQVDYIRVYK 382
                                                       203
                                                                                  293
                                                                                                               173
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                                                                                                                                                                                                   179
                                                                                                                                        234 -YGDNFHTFWFDWSPNGLRFFYDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYEND 292
                                                                                                                                                                                                                                                        119 RTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRS 178
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                                                                                                                                                                                                                                                                                                                                                                      5 LVVL-CLLFGEGFA---FTDWDQYHIVWQDEFDYFDGAKWQHEV--TATGGGNSEFQLYT
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                       KIQGGVNGKSAFRNKVFVILNMAIGGN-----
                                                                                                               TNGIDYHIYSVEWNSSIVKWFVNGN------
                                                                                                                                                                                          GEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLP-----KHSDDWN 233
                                                                                                                                                                                                                             YT-----SARLKTQFDKSWKYGKIEAKMAIPSFRGVWVMFWMSGDNTNYVRWPSS
                                                                                                                                                                                                                                                                                                        QDGANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCY 118
                                                                                                                                                                       GEIDFIE-----HRNTNNE----KVRGTIHW--
                                                                                                                                                                                                                                                                                      LVLLCCVVLHVGVARICCSHEPKWQLVWSDEFTNGISSDWEFEMGNGLNGWGNNELQYYR 61
                                                                               NPWAGGTNLAPEDQNEHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 209; DB 16;
Pred. No. 8.5e-11;
9; Mismatches 106
-MYIDYVRVYQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels 150;
                                                                                                             ----QYFEV
                                                                                                                                                                     -STPDGAHAHHNRESN
                                                      -WPGFDVADEA---
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                      239
                                                                                                             202
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Search completed: September 16, 2003, 11:25:56 Job time: 120.038 secs

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Minimum
Maximum
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: /cgn2_6/ptodata/1
6: /cgn2_6/ptodata/1
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Match
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Gapop 10.0 ,
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2240
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-98-580-4
US-09-98-580-4
US-09-311-6268-4
US-09-286-690-10
US-09-286-690-731-8
US-09-286-690-731-8
US-09-286-690-731-8
US-09-658-772-2
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US-08-712-072C-5
US-08-712-072C-2
US-08-392-828C-2
US-09-330-945-2
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US-09-159-106-2
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US-09-159-106-11
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US-08-392-828C-37
US-09-330-945-37
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  252-991A-32033
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11, Appl
4, Appl
4, Appl
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US-08-712-072C-3
Query Match
                                       ORGANISM:
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	90.5						92.5	92.5	92.5	92.5	92.5	93	93.5	94.5	94.5	95	96	96	
	4.0	4.0	4.0	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.2	4.2	4.2	4.2	4.2	4.3	4.3	
	429	429	242	386	386	386	371	371	371	371	312	829	1052	1278	276	1722	814	478	
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ALIGNMENTS	US-09-040-699A-4	US-08-745-977-4	US-09-286-690-11	US-09-795-583-5	US-09-739-861A-5	US-09-321-981-5	US-09-795-583-1	US-09-739-861A-1	US-09-321-981-1	US-09-104-308-1	·US-09-216-295-21	US-09-252-991A-27150	US-09-360-237-1	US-09-604-957-3	US-09-719-402A-6	US-09-194-612A-1	US-09-486-072-1	US-09-107-532A-4922	
	Sequence 4, Appli	Sequence 4, Appli	Sequence 11, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 21, Appl	Sequence 27150, A	Sequence 1, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 4922, Ap	

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Sequence 3, Application US/08712072C Patent No. 5925541
                                                                                                                                                                                            TELEFAX: (212) 286-0854
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
              STRANDEDNESS:
TOPOLOGY: Line
MOLECULE TYPE: P
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Elizabeth A
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 15m . COMPUTER: 15m . COMPUTER: SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: > CITY: New York
CITY: NY
TMATE: NY
TIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996
                                                                                                                                                           321 amino acids
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e13b,
                                                                                                       linear
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                                                                                                                                                                                                                                                  (212) 697-5995
                                                                        NO
                                                                                       peptide
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 Bacillus circulars
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Score 357;

DB 2;

Length 321;

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RESULT 2
US-08-392-828C-37
; Sequence 37, Application US/08392828C
; Patent No. 5795962
; Patent No. 5795962
                                    APPLICATION NUMBER: US/08/392.

APPLIANG DATE: 28-FEB-1995

CLASSIFICATION: 530

ATTORNEY/ACENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-1

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL POTITIES OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLRFFVDDE-----NQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLA 302
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                               262 amino acids
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SEKI, NORIAKI
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Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Applic
Patent No. 6077946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,945
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMEBOCYTE LYSATE FACTOR G SI
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IWANAGA, SADAAI
APPLICANT: MUTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                         COUNTRY: UZIP: 02110
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nes 100; Conserv
                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
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           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWTWDDEGDNNAMOVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFDQNFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIKWYVDGKFFYKVTNQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLRFFVDDE-----NQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG------TIHFGGQWPVNQ------SSGGDYHFPEGQTFANDYHVYSVVWEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTKDKLSLKYGRVDFRAKLPTGDGVWPALWMLPKDSVYGTWAASGEIDVMEARGRLPGSV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A-----NNDSKSFPQDP-----NRYAQYS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TMQVDYVRVYK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNFHTFWFDWSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09330945
                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          IWANAGA, SADAAKI
                                                                                                                                                                                                                                                                           PATENT ADMINISTRATOR, TESTA, HURWITZ
THIBEAULT, LLP
25 HIGH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%;
26.2%;
           09/119,995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 351.5; DB 1
Pred. No. 3.2e-27;
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                                                                                                                  #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - OWYSTAAPNNPN - -
                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 262;
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GENERAL INFORMATION:

APPLICANT: Perrer, Pau
APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Gluc
TITLE OF INVENTION: Activity
FILE REFERENCE: 4693,204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: 968-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1996-08-23
EARLIER FILING DATE: 1996-08-23
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: LOCATION: 1.262
: OTHER INFORMATION: /note= "BG1 A1 SEQUENCE (FIGURE 2)"
US-09-330-945-37
                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09159106 Patent No. 6284509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.7%; Score 351.5; DB 3; Best Local Similarity 26.2%; Pred. No. 3.2e-27; Matches 100; Conservative 44; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 PEDQNFHFILNVAVGGT--NGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 HIVWQDEFD--YFDGAKWQHEV-----TATGGGNSEFQLYTQDGANSFVRDGKLFIK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLRFFVDDE-----NQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWN-----YGDNFHTFWFDWSPN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWTWDDEGDNNAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIKWYVDGKFFYKVTNQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG-----TIHFGGQWPVNQ------SSGGDYHFPEGQTFANDYHVYSVVWEED 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFDEPFYLIMNLAVGGNFDGGRTP----NASDIPA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PITCHER, EDMUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 262;
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APPLICANT: Halkier, Torben
APPLICANT: Heddegaard, Lisbeth
TITLE OF INVENTION: An Enzyme With -1,3-Gluck
TITLE OF INVENTION: An Enzyme With -1,3-Gluck
TITLE OF INVENTION: Activity
FILE REPERENCE: 4693.204-US
CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0427/96
EARLIER APPLICATION NUMBER: 0885/96
EARLIER APPLICATION NUMBER: PCT/DK97/00160
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: PCT/DK97/00160
                                                                                  ; TYPE: PRT
; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-11
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US-09-159-106-11
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; TYPE: PRT
; ORGANISM: Oerskovia
US-09-159-106-13
  Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                              SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09159106 Patent No. 6284509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ferrer, Pau APPLICANT: Diers, Ivan
                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-04-14
                                                                                                                                           LENGTH: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 NINPOTGAPEGTDEMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFOKY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57. LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGYPDG--
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15.6%; Score 350; DB 3; Length 435; 28.5%; Pred. No. 9.4e-27; 
ive 30; Mismatches 96; Indels 1
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Conservative

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RESULT 6
US-08-712-072C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08712072C Patent No. 5925541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                       TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                             REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         NAME: Bogosian, Elizabeth A. REGISTRATION NUMBER: 39,911
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/712,072C FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                  STRANDEDNESS
                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                      TOPOLOGY:
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                                                                  amino acid
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; ORGANISM: gub, US-08-712-072C-4
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; ORGANISM: Oerskovia xanthineolytica
US-09-159-106-2
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Best Local :
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 263
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                                                                                             Query Match
Best Local
                                                                           Matches
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/159,106
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: 0427/96
EARLIER FILING DATE: 1996-12-04
EARLIER APPLICATION NUMBER: 0885/96
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: An Enzyme With -1,3-Glucanase TITLE OF INVENTION: Activity FILE REFERENCE: 4693.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ferrer, Pau
APPLICANT: Diers, Ivan
APPLICANT: Halkier, Torben
APPLICANT: Hedegaard, Lisbeth
                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-04-14
                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: PCT/DK97/00160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
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mes 112; Conserv
                                                                                               Local Similarity
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LLWSDEFDGAAGSAPNPAVWNHETGAHGWGNAELQNYTASRANSAL-DGQ--
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Pred. No. 1.
                                                                         Score 340.5; DB 3;
Pred. No. 4.1e-26;
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                                                                                                                 Length 263;
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Query Match 13.7%; Score 307; DB 2; Length 306; Best Local Similarity 26.2%; Pred. No. 1.2e-22; Matches 95; Conservative 36; Mismatches 97; Indels 134; Gaps 13;	; LENGTH: 306 amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-824-707-2	TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123 TELEPHAX: 212-867-9655 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	ril-199 5 ATION: a A. : 35,1	M PC CON STEM: PC Atentin F ATION DAI	STATE: New York STATE: New York COUNTRY: U.S.A. ZIP: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	CORRESPONDENCE ADDRESS:  ADDRESSEE: No. 59196880 No. 5919688disk of No. 5919688th America, Inc.  STREET: 405 Lexington Avenue, Suite 6400	; APPLICANT: ASELJO, Juna ; APPLICANT: Savva, Demitris ; TITLE OF INVENTION: No. 5919688el enzyme with beta-1,3-glucanase activity ; NUMBER OF SEQUENCES: 4	Diers, I Hedegaar Halkier,	5919688 FORMATION: T: Ferrer, F	US-08-824-707-2 ; Sequence 2, Application US/08824707	RECTION 8	237	GTTQLPQOMKV	QY 321 GFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRV 380	QY 261 LLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTN 320		141 80	Qy 81 NINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140
: TOPOCHOGY: linear ; MOLECULE TYPE: peptide ; HYPOTHETICAL: NO	710-581-4766 710-581-4766 SEQ ID NO: 5: STERISTICS: amino acids acid	REGISTRATION NUMBER: 39,911 ; REGISTRATION NUMBER: 363475/97 ; REFERENCE/DOCKET NUMBER: 63475/97 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212) 697-5995 ; TELEPHONE: (212) 686-6854 or 286-6089	CLASSIFICATION 485 ; CLASSIFICATION DATA: ; PRIOR APPLICATION DATA: ; PAPULICATION UMBER: ; FILING DATE: ; FILING DATE: ; FILING DATE: ; ATTORNEY/AGENT INFORMATION:	NAN	STATE: NY COUNTRY: US ZIP: 10016 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE COMPUTER: IBM PC COMPATIBLE		; APPLICANT: Jack Goldstein, Alex Zhu and Lin Leng ; TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE ; NUMBER OF SEQUENCES: 13 ; CORRESPONDENCE ADDRESS:	plication US/08712072C 5541 MATION:	RESULT 9	Db 300 VY 301	Qy 380 VY 381	QY         320 NGF I PDGC I NRGCI PALOKHWINGDWY NDAMRK F PDARGNWKWTWDDEGDNAMQ V DY IR 379           Db         278QWPGNPDATTPFP	247 EYHRVTTADVGANQW	Qy 260 ALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGT 319	Qy 201 GIQKMGSTMHWGPGWD-DNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQ 259	Qy141 SFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDEKNTGGEEL 200	QY 81 NINPQTGAPFGTDFMYNGYLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKY 140	Qy 26 IVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLAD 80 :

Length Indels 155;

422;

Gaps

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US-08-712-072C-2
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ORIGINAL SOURCE:
ORGANISM: Flavobacterium Keratolyticus
US-08-712-072C-5
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Best Local Similarity
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                                                                                                               FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb
COMPUTER: IBM PC COMPATIBLE
         ATTORNEY/AGENT INFORMATION:
NAME: BOGOSIAN, Elizabeth A.
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ENDO-BETA-GALACTOSIDASE NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 11-SE
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
STREET: 9
                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNL
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                                                                                                                                                                                                                                                                                                      SD
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(212) 286-0854 or 286-0082
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27.0%;
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                                                                                                                                                                                US/08/712,072C
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Pred. No. 1.2e-20;
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                                                                                                                                                                                                                                                          STORAGE DISKETTE
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US-08-392-828C-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                 Sequence 2,
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                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                           APPLICANT: MUTA, TATSUSHI
APPLICANT: SEKI, NORIAKI
APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: THERE
                                                                     ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR,
ADDRESSEE: THIBEAULT
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ORIGINAL SOURCE:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                      COUNTRY:
                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                      , Application 5795962
                                                                                                                                  BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPAMSARVRTFQKYSFTHGRVVVHAK-----MPV---GDWLWPAIWMLPED-WVYGGWPR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTNLAPFDQNFHFILNVAVG-GTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDA 356
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                                                                                                                      MA
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               Version
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                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09330945 Patent No. 6077946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  APPLICANT:
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJJ
TELECOMMUNICATION INFORMATION:
                                                                                                                          APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: DNA ENCODING HORSESHOE CRAB
TITLE OF INVENTION: AMERICANTE LYSATE FACTOR G SI
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESSE: PATENT ADMINISTRATOR, TESTA, HURWIT
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                        STATE: MA
COUNTRY: USA
                                                                                           CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 AVGGTNGFIPDGCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQ 374
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                                        02110
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Similarity 21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              IDYVRVYQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNV 314
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MUTA, TATSUSHI
SEKI, NORIAKI
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Pred. No. 2.9e-12;
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                                                                                                                                          TESTA, HURWITZ
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                                                                                                                                                                                               G SUBUNIT
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RESULT 13
US-08-737-526-4
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                                                                                                                                   Sequence 4, Application
Patent No. 5871966
GENERAL INFORMATION:
APPLICANT: Kofod, L
APPLICANT: Andersen
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Best Local S
Matches 79
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              CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58719660 No.
                                                 APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Christgau, Stephan
TITLE OF INVENTION: An Enzyme With Endo-1,3(4)-B-Glucanase
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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amino acid
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IDYVRVYQ 234
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                                                                                                                                                                                                         Application US/08737526
405 Lexington Avenue
                                                                                                                                   Kofod, Lene Venke
Andersen, Lene No.
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21.5%; Pred. No. 2.
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                   5871966disk of No.
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.9e-12;
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                 5871966th America,
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US-09-098-580-4
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Best Local S
Matches 85
                         GENERAL INFORMATION:
APPLICANT: Kofod, I
APPLICANT: Andersen
APPLICANT: Kauppin
APPLICANT: Christga
                                                                                                 Sequence 4, Application US/09098580 Patent No. 6140096
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,526
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION:
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TYPE: amino acid
STRANDEDNESS: sir
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                      Andersen, Lene No. 61400
Kauppinen, Markus Sakari
Christgau, Stephan
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                                                                      Rofod, Lene Venke
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An Enzyme With Endo-1,3(4)-B-Glucanase Activity
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RESULT 15
US-07-985-458-3
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Best Local s
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61400960 No. 6140096disk of
STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/7:
FILING DATE: 08-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Valeta, Gregg A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATE FAST-SEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TELEPHONE: 212-878-9655
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ZIP: 10174-6401
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STATE: NY
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                                                                                                                                                                                                      DNFHTEWEDWSPNGLREEVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQYENDNPW 295
                                                                                                                                                                                                                                    V---DGQATGHGTLHCDVYPGGICNEGNGI-GGPVNIANVNDWHAWRVEIDRTPSSW---
                                                                                                                                                                                                                                                  IGNRDEKNTGGEEL-----GIQKMGSTMHWGP----GWDDNRYWLTSLPKHSDDWNYG 235
                                                                                                                                                                                                                                                                                         KYTFTPAAGKVTRLEAAIRFGSNAQANKQGIWPAFWMLGDSLRQPGGSWPNCGEIDIMET 165
                                                                                                                                                                                                                                                                                                           KYSFT--HGRVV-VHAKMPVG------DWLWPAIWMLPEDWVY--GGWPRSGEIDIIET 186
                                                                                                                                                                                                                                                                                                                                                    --QLVPWRDSSKGT-
                                                                                                                                                                                                                                                                                                                                                                            ADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQ 138
                                                                                                                                                                                                                                                                                                                                                                                                              FNLVWTDTFAGNGGTSPNQNNW-NIITGNLNVNAEQETYSSSTANVQLSGGS-----TL-
                                                                                                                                                                           ---QSETLTWSLDGTIYFQITGS-----
                                                                                                                   ---NNIA--HSPLFFILNVAVGG-----
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22.0%; Pred. No. 7e-
ative 40; Mismatches
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Sequence 3, Application US/07985458 Patent No. 5344777

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/985,458
FILING DATE: 19921203
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/658,221
FILING DATE: 20-FB8-1991
APPLICATION NUMBER: 73440/1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                     STRAIN: MH-24
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (212)972-1400
TELLEPAX: (212)370-1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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SOFTWARE: ASCII FORM
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TELEX: 236268
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                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 738 amino acids TYPE: amino acid TOPOLOGY: unknown
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                                Beppu, Teruhiko
Cloning and Sequencing of the Gene Cluster
Encoding Two Subunits of Membrane-Bound
Alcohol Dehydrogenase from Acetobacter
                  polyoxogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 Third Avenue
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Fukaya, Masahiro;
                                                                                                       Nishiyama, Makoto;
Horinouchi, Sueharu and
                                                                                                                                                              Okumura, Hajime;
                                                                                                                                                                                 Takemura, Hiro
Tayama, Kenji;
Biochimica et Biophysica Acta.
                                                                                                                                               Kawamura, Yoshiya;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamakí, Toshimi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible (NEC PC-9801 ES)
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                                                                                                                                                                                                  Hiroshi;
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US-07-985-458-3
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Best Local Similarity 20.4
Matches .78; Conservative
                                                                                                         245
                                                                                                                                             428
526 TGGDLLFQGLANGEFHAYDATNG
                                 302 APEDQNEHFILN---VAVGGTNG
                                                                     483 DSPEAKQAFVKDLK-----
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                                                                                                                                                                                                                379 AKTGEFI-----SGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGD 427
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                                                                                                                                                                                                                                                                                                                                                              259
                                                                                                                                                                                                                                                    153 MPVGDWLWPAIWMLPEDWVYGGW-----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K 204
                                                                                                                                                                                                                                                                                                                        126 ----IPPAMSARVRTFQ-----KYSFTHGR----------VVVHAK------ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                   212 GNGGSEF-----GARGFVSAFDAETGKVDWRFFTVP-----NPKNEPDAASDSVLMN
                                                                                                                                                                                                                                                                                                                                                                                                98 GVLDVWAMYGACTNTDNNGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GGGNSEFQLYTQDGANSFVR------DGKLFIKPTLLADNINPQTGAPFGTD-FMYN
                                                                                          WSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE---WGKPWLPQYENDNPWAGGTNL 301
                                                                                                                                           LGGHNFAAMAFSP-----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIP 482
                                                                                                                                                                             MG----STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                                                                                                                                                            KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112.5; DB 1;
Pred. No. 0.013;
7; Mismatches 113;
548
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                                                                       -----GWIVAWDPQKQAEAW--RVDHKGPWNGGILA 525
                                                                                                                                                                           ----KHSDDWNYGDNFHTFWFD
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Search completed: September 16, 2003, 11:30:26 Job time: 42.6247 secs

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Title:
Perfect score:
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                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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1 MRWTLVVLCLLEGEGFAFTD......DDEGDNNAMQVDYIRVYKRN 384
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DHET_ACEPO
XYNA_RUMFL
GUB_BACLI
NANH_VIBCH
KRE6_YEAST
GUB_PAEPO
DHET_ACEEU
OSTA_HAEIN
XYND_RUMFL
GUB_CLOTM
FDXG_HAEIN
XYNX_CLOTM
FDXG_HAEIN
XYNX_CLOTM
ANYB_PAEPO
XYNA_THESA
YY07_METJA
EXAA_PSEAE
GLGB_ECOLI
SKN1_YEAST
BRU1_SOYBN
MS1P_CRIGR
MOKB_SCHPO
TREZ_MYCTU
MANB_ASPNG
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AGGAA_VIBS7
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P23903 bacillus ci
P45798 rhodothermu
033680 rhizobium m
09z3q2 rhizobium m
09z3q2 rhizobium m
09z3q2 rhizobium m
P28036 acetobacter
P29126 ruminococcu
P27051 bacillus li
P37060 vibrio chol
P32486 saccharomyc
P45797 paenibacil
044002 acetobacter
P44846 haemophilus
053317 ruminococcu
P07980 bacillus am
P87023 candida alb
P29716 clostridium
P46448 haemophilus
P87044 candida alb
P29716 clostridium
P35435 clostridium
P3544 paenibacill
P3637 thermoanaer
060306 methanococc
09z4j7 pseudomonas
P07766 asccharomyc
9z496 glycine max
009854 schizosacch
032694 glycine max
092854 schizosacch
010769 mycobacteri
09uza aspergillus
09wtza rattus norv
P20910 streptomyce
P48839 vibrio sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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E13B_BACCI
ID E13B_BACCI
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-	GUNH_CLOTM	ACON_GRAVE	DESA_SPIPL	ISOA_PSESP	ISOA_PSEAY	GUB_BACBR	COX1_BRAJA	APE3_YEAST	FIBB_HUMAN	AGAR_STRCO	KRE2_CANAL	FM2_ACTNA
	P16218 clostridium	P49609 gracilaria	Q54794 spirulina p	P26501 pseudomonas		P37073 bacillus br			P02675 homo sapien		_	P12616 actinomyces

## ALIGNMENTS

В	Qγ	Qu Be Ma	SPTT	K D D R	DR DR	388	888	888	នួន	ខ្លួន	14 S S	Ŗ Ŗ	R R R R	R RP	R O C	8 8 8	DE DE	D D	PA E
424 NLIWQDEFNGTTLDTSKWNYETGYYLNNDPATWGWGNAELQHYTNSTQNVYVQDGKLNIK 483	IVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSF	Query Match 15.7%; Score 351.5; DB 1; Length 682; Best Local Similarity 26.2%; Pred. No. 2.2e-21; Matches 100; Conservative 44; Mismatches 89; Indels 149; Gaps 14;	CHAIN 39 682 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1. ACT_SITE 552 552 NUCLEOPHILE (BY SIMILARITY). ACT_SITE 557 557 PROTON DONOR (BY SIMILARITY). SEQUENCE 682 AA; 75465 MW; BC4F407E34D4ADD5 CRC64;	PF00722; Glyco_ E; PS01034; GLY all; Hydrolase;	16.	ısb-sib.	institutions as long as its content is in no tatement is not removed. Usage by and for commerc	ISS-PROT entry is copyright. It is the Swiss Institute of Bioinforma ppean Bioinformatics Institute. Th	-!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.		Gene 86:113-117(1990)i- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1, 3-GLUCANS. TMPLICATED IN THE DEFENSE AGAINST FUNCAL BATHOGENS	"Structure of the gene encoding beta-1,3-glucanase Al of Bacillus circulans WL-12.";	MEDIANE-90185240; PUDMEC=2311931; Yahata N., Watanabe T., Nakamura Y., Yamamoto Y., Kamimiya S., Tanaka H.;		ncbl_TaxID=1397; [1]	circulans.	an endo-1,3-b -glucan endoh	-1991 (Rel. 20, Last sequence update) -1999 (Rel. 38, Last annotation update)	El3B_BACCI STANDARD; PRT; 682 AA. P23903; 01-NOV-1991 (Rel. 20. Created)

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Spilliaert R., Hreggvidsson G.O., Kris
Eggertsson G., Palsdottir A.;
"Cloning and sequencing of a Rhodother
for a thermostable beta-glucanase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4,1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GUB_RHOMR P45798;
                     Hydrolase;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Bacteroidetes;
Crenotrichaceae; Rhodothe
NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodothermus marinus (Rhodothermus obamens Bacteria; Bacteroidetes; Sphingobacteria;
   CHAIN
                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                             modified
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                                                                              Ptam;
                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                 J. Biochem. 224:923-930(1994).
FUNCTION: SHOWS ACTIVITY ON LICHENAN, BETA-GLUCAN AND LAMINARIN BUT NOT ON CMC CELLULOSE OR XYLLAN.
CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
MISCELLANEOUS: The enzyme has temperature optimum of 85 degrees Celsius and a pH optimum of 7.0.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict
                                                                                                               S48201;
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                                                                                                                                 U04836;
                                                          S48201; S48201.
PFO; IPRO00757; Glyco_hydro_16.
PF00722; Glyco_hydro_16; 1.
TE; PS01034; GLYCOSYL_HYDROL_F1
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                                       Glycosidase;
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Query Match
                                             Finan T.M., Weldner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowle A., Golding B., Puehler A., "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti."; Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                                                                                                                                                        "The Rhizobium meliloti exoK gene and prsD/prsE/exsH components of independent degradative pathways which production of low-molecular-weight succinoglycan."; Mol. Microbiol. 25:117-134(1997).
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endo-1,3-1,4-beta-glycanase exsH (EC 3.2.1.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-21899394; PubMed-11902715;
York G.M., Walker G.C.;
"The Rhizobium meliloti exoK gene
                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthesis protein exsH) EXSH OR RB1055 OR SMB20932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXSH_RHIME O33680;
                CHARACTERIZATION.
                                                                                                                                                                         STRAIN-1021
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                 Rhizobiaceae;
MEDLINE=98226741;
                                                                                                                                                     MEDLINE=21396508;
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112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRWTLVVLCLLFGEGFAFTD------WDQYHIVWQDEFDYF---DGAKWQHEVTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRRTAFLLSVLIGCSMLGSDRSDKAPHWE---LVWSDEFDYSGLPDPEKWDYDVGGHGWG
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163
286
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                                                                                                                   ; PubMed=11481431;
ner S., Wong K., B
Hernandez-Lucas I
PubMed=9560202;
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163
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PROTON DONOR (BY SIMILARITY).
; 7215C33624135191 CRC64;
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96;
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contribute to
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RESULT 4
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Best Local :
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EMBL; AL603645; CAC49455.1; -.
PIR; G95973; G95973.
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF007353; hemolysinCabind; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00313; CABNDNGRPT.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG.

PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.

Exopolysaccharide synthesis; Glycosidase; Hydrolase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Exopolysaccharide biosynthesis.
SUBCELLULAR LOCATION: SECRETED. PROBABLY BY A TYPE-III SYSTEM.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                    364
                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                 27 VWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLADNINPQT
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                                                                             GL--
                                                                                                   GCINRGGDPALQKPWSNGDWYNDAMRKFFDARGNWKWTWDDEGDNNAMQVDYIRVY 381
                                                                                                                                                                                IATVH--SNETGSRTSIENSVKVAD----ASGFHTYGVLWTEEEIVWYFDDAAIARADTP
                                                                                                                                                                                                          GSTMHWGPGWDDNRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVP 265
                                                                                                                                                                                                                                                 YPLIDANPWWVDFWEWGKPWLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPD
                                                                                                                                                                                                                                   YFEMRADMPDDQGVWPAFWLLPAD---GSWP--PELDVVEMRGQD--SNT------V
                                                                                                                                                                                                                                                                                       Walker G.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 AA;
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349
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             STANDARD
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349
354
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21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 175.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC:
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                               102;
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                                                                            -ADGSEMKIDYIKAY
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Query Match
Best Local S
Matches 82
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RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizoblum meliloti pSymA megaplasmid.";
RI Proc. Natl. Acad. Sci. U.S.A. 98.9883-9888 (2001).
- FUNCTION: CLEAVES HIGH MOLECULAR WEIGHT SUCCINOGLYCAN TO YIELD LMW
C. SUCCINOGLYCAN. DYMAMICALLY REGULATES THE MOLECULAR WEIGHT
DISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN
ONLY DURING A LIMITED PERIOD AFTER ITS SYMTHESIS, PEHAAPS BEFORE
C. IT UNDERGOES A TIME-DEPENDENT CHANGE IN ITS CONFORMATION OR
C. AGGREGATION STATE (BY SIMILARITY).

C. PATHMAY: EXOPOLYSACCHARIDE DISSYNCHESIS.
--- SUBCELLULAR LOCATION: SECRETED. PROBABLY BY A TYPE-III SECRETION
SYSTEM (BY SIMILARITY).
                                                                                           DOMAIN
ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                               EMBL; AJ225896; CAB38101.1; -.
EMBL; ASE007273; AAK65522.1; -.
PIR; H95369; H95369.
InterPro; IPR000757; Glyco_hydro_16.
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF007353; hemolysincabind; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CXM1-105;
MEDLINE-99413305; PubMed-10485295;
Sharypoya L.A., Yurgel S.N., Kelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
28-FEB-2003 (Rel. 41, Last amotation update)
28-FEB-2003 (Rel. 41, Last amotation update)
28-FEB-2003 (Rel. 41, Last amotation update)
Endo-1,3-1,4-beta-glycanase eglC (EC 3.2.1.) (Succinoglycanasynthesis protein eglC).
EGLC OR RA0866 OR SMA1587.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                           SEQUENCE
                                                                                                                                                                                                          PRINTS; PR00313; CABNDNGRPT.

PROSITE; PS01034; GLYCOSYL_HYDROL_F16; FALSE_NEG.

PROSITE; PS00330; HEMOLYSIN_CALCIUM; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The eff-482 locus of Sinorhizobium meliloti CXMI-105 that influences symblotic effectiveness consists of three genes encoding an endoglycanase, a transcriptional regulator and an adenylate cyclase."; mol. Gen. Genet. 261:1032-1044(1999).
                                                                                                                                                                      Complete
                                                                                                                                                                                        Exopolysaccharide synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barnett M.J., Fisher R.F., Jones T., Komp C., Abo
Barloy-Hubler F., Bowser L., Capela D., Galibert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=382;
 l Similarity
82; Conserv
                                                                                                                                                                        proteome.
                                                                         465 AA;
                                                                                               349
354
52
                                                                         49614 MW;
               7.5%;
22.7%;
                 Score 167; DB 1
Pred. No. 2e-06;
                                                                         PROTON DONOR (BY SIMILARI
I -> T (IN REF. 1)
; 12CB879AED9E6558 CRC64;
                                                                                                                                                                                        Glycosidase;
                                                                                                                                                    CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keller
                                                                                                                                NUCLEOPHILE (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Komp C., Abola A.P.,
                                                                                                                                                                                        Hydrolase;
                                   1:
                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Succinoglycan
                                   Length 465
                                                                                                                                                                                          Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Puehler
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Conservative

40;

Mismatches

117;

Indels 122;

Gaps

19;

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01-AUG-1992
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACEPO
                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: POO AND HEME.
-!- SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, GRALLER UNKNOWN SUBUNITS) THAT FORMS THE
                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted by the company of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHET_ACEPO P28036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bactería; Proteobactería;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alcohol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91159482; PubMed=2001402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetobacter polyoxogenes.
                                                                                                                                                                                                                 SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING SPACE (POTENTIAL).
SIMILARITY: BELONGS TO THE BACTERIAL POO DESIMILARITY: Contains 1 cytochrome c domain.
                                                                                                                                                                                                                                                                                                              COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                reduced acceptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FANTSADQLHANQFSLALDRSVLTQTFSDDFNTLQLSDGTSGVWDPKYWWAPEKGATLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGFIPDGCINRGGDPALQ--KPWS-NGDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDDWNYGDNFHTFWFDWSPNGLRFFYDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPE
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2 (Rel. 23,
3 (Rel. 41,
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  BAA00528.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGFHKYGVLWTEEEIVWYFDDAAIARADTPSDMHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update;
Last annotation updat
[acceptor] precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MLVNLAIGGMAGPPTDGLMG-GAEMKVDYVKAYSLDADW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SGMLTTYSSFAQTYGYFEMRADMPDDQGAWPAFWLLPG
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                                                                                                      There are no restrictions ong as its content is in
                                                                                                                                                                                                                                          PQQ DEHYDROGENASE
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                                                                                                                                                                                                                                                                                                                                CYTOCHROME, AND TWO
E ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodospirillales;
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Best Local S
Matches 78
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BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001479; Bac_PQQ.
InterPro; IPR002372; Bac_PQQ_repeat.
InterPro; IPR000345; CytC_heme_bind
pfam; PF01011; Bacterial_PQQ; 3.
SMART; SM00564; PQQ; 3.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q9Z4J7;
                                                                    302
                                                                                        483
                                                                                                                                 428
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                                                  526
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                                                                                                                                                                                                                                                                                                                                       78; Conser
                                                 TGGDLLFQGLANGEFHAYDATNG
                                                                                                                                                                                                                                                       KAYQTWSPTGAWTRQGGGGTVWDSIVYDPVADLVYLGVGNGSPWNYKYRSEGKGDNLFLG
                                                                                                                                                                                                                                                                           GVLDVWAMYGACTNTDNNGC----
                                                                                                                                                                                                                                                                                                GNGGSEF---
                                                                                                                                                                                                                                                                                                                   GGGNSEFQLYTQDGANSFVR------DGKLFIKPTLLADNINPQTGAPFGTD-FMYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00190;
                                                                                                                                                   MG----STMHWGPGWDDNRYWLTSLP-----
                                                                                                                                                                                                                SIVALKPETGEYVWHFQETPMDQWDFTSDQQIMTLDLPINGETRHVIVHARKNGFFYIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00363;
                                                                   APFDQNFHFILN---VAVGGTNG
                                                                                         DSPEAKQAFVKDLK --
                                                                                                            WSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE---WGKPWLPQYENDNPWAGGTNL
                                                                                                                                                                        AKTGEFI-----SGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGD
                                                                                                                                                                                            MPVGDWLWPAIWMLPEDWVYGGW-----PRSGEIDIIETIGNRD--FKNTGGEFLGIQ-K
                                                                                                                                                                                                                                     ---- IPPAMSARVRTFQ-----KYSFTHGR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00364;
                                                                                                                                LGGHNFAAMAFSP-----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIP
                                                                                                                                                                                                                                                                                                                                                                             1
36
634
650
653
654
738
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                AA;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACTERIAL_PQQ_2;
CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIAL_PQQ_1;
                                                                                                                                                                                                                                                                                                                                                                                         738
738
650
653
                                                                                                                                                                                                                                                                                                                                                                                80840
                                                                                                                                                                                                                                                                                                                                                5.0%;
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                                                                                                                                                                                                                                                                                               -GARGFVSAFDAETGKVDWRFFTVP-----
                                                                                                                                                                                                                                                                                                                                                                                 Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Periplasmic;
                                                                                                                                                                                                                                                                                                                                       37;
                                                                                                                                                                                                                                                                                                                                      Score 112.5;
Pred. No. 0.09
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         IRON
                                                                                                                                                                                                                                                                                                                                                                                                             HEME
                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOCHROME C-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALCOHOL DEHYDROGENASE [ACCEPTOR]
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
PRT;
                                                                                                                                                                                                                                                                                                                                                                             ON (HEME AXIAL LIGAND)
1E2B6ED7BCD92AF6 CRC64;
                                                  548
                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                                  (COVALENT) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --
                                                                                                                                                                                                                                                                                                                                                  112.5; DB
954
                                                                                          -GWIVAWDPQKQAEAW--RVDHKGPWNGGILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane;
8
                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                        113;
                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                     ----KHSDDWNYGDNFHTFWFD
                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                            ----YRTGAAGD----
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                                                                                                                                                                                                                                    - VVVHAK - - - -
                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                        155;
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                          525
                                                                                                                                 482
                                                                                                                                                     244
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                                                                                                                                                                                            204
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                                                                                                              301
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RESULT 6

XYNA_RUMFL
IDN XYNA_R
AC P29126
DT 01-DEC
DT 28-FEB
DE Bifunc
GN XYNA.
OS Ruminc
OC Bacter
OC Ruminc
OX NCEL_T
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RX Zhang
RT cellul
RT cellul
                                                                                                                                                                                                                                   XYNA_RUMFL
P29126;
01-DEC-1992
01-DEC-1992
28-FEB-2003
MEDLINE=92261318; PubMed=1584021;
Zhang J.-X., Flint H.J.;
"A bifunctional xylanase encoded by the xynA gene of the rumen
"A bifunctional xylanase encoded by the xynA gene of the rumen
cellulolytic bacterium Ruminococcus flavefaciens 17 comprises two
dissimilar domains linked by an asparagine/glutamine-rich sequence.";
                                                                                    SEQUENCE FROM N.A. STRAIN=17;
                                                                                                                                                                                                                   Bifunctional
                                                                                                                                    NCBI_TaxID=1265;
                                                                                                                                                     Ruminococcus
                                                                                                                                                                     Bacteria;
                                                                                                                                                                                      Ruminococcus
                                                                                                                                                                     Firmicutes;
                                                                                                                                                                                                                  (Rel. 24, Created)
(Rel. 24, Last sequence up
(Rel. 41, Last annotation)
l endo-1,4-beta-xylanase X
                                                                                                                                                                                    flavefaciens
                                                                                                                                                                     Clostridia;
                                                                                                                                                                     Clostridiales;
                                                                                                                                                                                                                   XYLA precursor
                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                     Lachnospiraceae
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Best Local S
Matches 77
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ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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SMART; SN00633; GlYCO_SYL_HYDROL_F10; 1.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO01000; Glyco_hydro_10.
InterPro; IPRO01137; Glyco_hydro_11.
Pfam; PP00331; Glyco_hydro_10; 1.
Pfam; PP00457; Glyco_hydro_11; 1.
PRINTS; PR00134; GLHYDRLASE10.
PRINTS; PR00911; GLHYDRLASE11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linkages in xylans.

PATHWAY: Xylan degradation.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS
G (FAMILY 11 OF GLYCOSYL HYDROLASES).

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS
F (FAMILY 10 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microbiol. 6:1013-1023(1992).
FUNCTION: XYLANASE DOMAIN 1 RE
AND DOMAIN 2 MORE XYLOSE.
                                                    278
                                                                                                 325
                                                                                                                                            218
                                                                                                                                                                                         274
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; P48793; 1XND.
                                                                                                                                                                                                                                                                                                                                                                           168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                      80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
77; Conserv
                                        FWEWGKPWLPQYEN-DNPWAGGINLAPFDQNFHFILNVAVGGINGFIPDGCINRGGDPAL
                                                                                                                                                                                                                                                                                                                                                               TATFPQYWSVRQTSGSANNQTNYM-KGTIDVTKHFDAWSAAGLDMSGTLYEVSLNIEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYHIV--WQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSF-VRDGKLFIKPTLLA
                                                                                                                    NRYWLTSLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVD
                                                                                                                                                                                                                          LPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGE-----FLGIQKNGSTMHWGPGWDD
                                                                                                                                                                                                                                                                       YRSNGSANV----KSVSVTQGGSSDNG-----GQQQNNDWNQQNNNQQQNNDWNWGQ
                                                                                                                                                                                                                                                                                                                    CYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAKMPVGDWL-------WPAIWM
                                                                                                                                                                                                                                                                                                                                                                                                          DNINPQ-----TGAPFGTDFMYNGVLDV-----WA-----MYGACTNTDNNG
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  NNDWNQ-WNNQNNNQQNAWNGWDNNNNWNQN-
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954
622
954
122
774
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19.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              WR-----PPGNDGEVKGTVSANGNTYDIRKTMRYNQPSLDG
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XYLANASE DOMAIN 1.
ASN/GLN/TRP-RICH (I
XYLANASE DOMAIN 2.
NUCLEOPHILE (BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112.5; D
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOPHILE
                                                                                                                                                                                  -QNNDWNNWGQQNNDWNQWNNQGQQQNNDWNNWGQQNND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152;
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NOOONNWDWNN
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                                                                                       DWNNWGQQ
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                                                                                       369
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RESULT 7
GUB_BACLI
  JB; 1GBG; \\
InterPro; IP
Pfam; Pro
PFro
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01-AUG-1992 (Rel. 23, Createw,
01-AUG-1992 (Rel. 23, Last sequence update,
01-BUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and find this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Juncosa M., Pons J., Dot T., Querol E., Planas A.; "Identification of active site carboxylic residues in E licheniformis 1,3-1,4-beta-D-glucan 4-glucanohydrolase site-directed mutagenesis."; J. Biol. Chem. 269:14530-14535(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUB_BACLI
P27051;
01-AUG-1992
                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hahn M., Pons J., Planas A., Querol E., Heinemann U., "Crystal structure of Bacillus licheniformis 1,3-1,4-beta-D-glucan glucanohydrolase at 1.8-A resolution."; FEBS Lett. 374:221-224(1995).
                                                                                                                                                               entities requires a 
or send an email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glucanohydrolase from mutagenesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96063718; PubMed=7589539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92362869; PubMed=1354172; Planas A., Juncosa M., Lloberas J., "Essential catalytic role of Glul34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Queroi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS Lett.
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Lloberas J., Perez-Pons J.A., Que
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
MISCELLANEOUS: BETA-GLUCANASES OF BACILIUS HAVE A SUBSTRATE RANGI SIMILAR TO LICHENASE OF GERMINATING BARLEY.
SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
; PF00722; GI
rs; PR00737;
                                                                                       ; X57279; CAA40547.1;
S15388; S15388.
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                                                                                                                                                          an email to license@isb-sib.ch).
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                                          IPR000757;
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                                                                07-DEC-95.
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00757; Glyco_hydro_16
Glyco_hydro_16; 1.
7; GLHYDRLASE16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. licheniformis
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in endo-beta-1,3-1,4-D-glucan 4-
mis as determined by site-directer
                                                                                                                                                                                      (See http://www.isb-sib
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                     SLGEMRLSLTSPSYNKFDCGENRSVQTYGYGLYEVNMK---
                                            LFLSLSTFAASASAQTGGSFYEPFNNYN--TGLWQKADGYSNGNMFNC
                                                       LFIKPTLLADNINPQTGAPFGTDF-MYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPA
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21.9%;
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26 % OF WILD-TYPE ACTIVITY.

27 % OF WILD-TYPE ACTIVITY.

28 % OF WILD-TYPE ACTIVITY.

29 % OF WILD-TYPE ACTIVITY.

20 COMPLETE LOSS OF ACTIVITY.

21 COMPLETE LOSS OF ACTIVITY.

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28-FEB-2003 (Rel. 41)
Sialidase precursor (
NANH OR VC1784
LT 8
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Wasserman S.S., Kaper J.B.
"Role of Vibrio cholerae not
toxin.";
                                                                                                                                                          Taylor G.L., Vimr "Purification, cr of neuraminidase
                                                                                                                                                                                                                                                                                                                                                    Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
                                                                                 "Crystal structure of Vibrio
                                                                                                                                                                                                                        Vimr E.R., Lawrisuk L., Galen J.E., Ke "Cloning and expression of the Vibrio nanH in Escherichia coli";
J. Bacteriol. 170:1495-1504(1988).
                                                                                                                                                                                                                                                                SEQUENCE OF 1-44 I
STRAIN=Classical C
MEDLINE=88169467;
                                                                                                                                                                                         CHARACTERIZATION,
MEDLINE=92389334;
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Fraser C.M.;
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MEDLINE=20406833; PubMed=10952301;
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STRAIN=El Tor N16961
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MEDLINE=92112298;
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Vibrionaceae;
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                                                                                                      MEDLINE=95006320; PubMed=7922030;
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                                                                                                                                        Mol. Biol.
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                                                                                                                 CRYSTALLOGRAPHY (2
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eae; Vibrio.
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(Rel. 41, Last annotation
recursor (EC 3.2.1.18) (Neu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
                                                                                                                                                           Vimr E.R., Garman E.F., Laver W.G
n, crystallization and preliminary
dase from Vibrio cholerae and Salmo
                                                                                                                                       226:1287-1290(1992).
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Ogawa 395 / ATC
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PubMed=1730470;
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cholerae
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W.C., White O.,
.J., Venter J.C.
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C MICROBIAL INFECTIONS. NANH FACILITATES CHOLERA TOXIN BINDING
C TO HOST INTESTINAL EPITHELIAL CELLS BY CONVERTING CELL SURFACE
C POLYSIALOGANGLIOSIDES TO GMI MONOGANGLIOSIDES
C -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
C alpha-(2->8)-glycosidic linkages of terminal sialic residues in
C oligosaccharides, glycoproteins, glycolipids, colominic acid and
C synthetic substrates
C -!- CACTOR: CALCIUM.
C -!- SUBUNIT: MONOMER (Probable).
C -!- SUBCELLULAR LOCATION: Secreted.
C -!- SUBCELLULAR LOCATION: Secreted.
C -!- INDUCTION: MAY BE CONTROLLED BY SIALIC ACID AVAILABILITY AND A
C GROWTH-HASE-DEPENDENT MECHANISM.
C -!- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
-!- SIMILARITY: CONTAINS 4 BNR repeats.
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EMBL; M82625; AAF94933.1; ALT_INIT.
EMBL; M19268; AAA27547.1; --
PIR; A27734; A27734.
PIR; A43866; A43866.
PDB; 1KIT; 05-JUN-97.
TIGR; VC1784; --
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                           InterPro; IPR002860; GH_BNR.
Pfam; PF02012; BNR; 4.
Hydrolase; Glycosidase; Sign
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   Signal; Repeat;
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BNR 1.
BNR 2.
BNR 3.
BNR 4.
PROTON DONOR (BY SIMILARITY).
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                    82;
                           Similarity
                    Conservative
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394
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413
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428
434
438
                                             4.9%;
                   ; Score 109; DI
; Pred. No. 0.2;
31; Mismatches
                         DB 1;
.2;
                   107;
                              Length 781;
                   Indels 128;
                   Gaps
                   20;
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Prince Pr

cerevisiae chromosome XVI.";

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RESULT 9

KRE6_YEAST

ID KRE6_Y

AC P32486

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             Hall J., Hebling U., neumann R., Johnston M., Kalman S., Kleine K.,
Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
Ulrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
walsh S.V. Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
                                                                                                                               MEDLINE-97313271; PubMed-9169875;
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis R., Davis R.W., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietaltrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau Hall J., Hebling U., Heumann K., Hilbert H., Hillier L., Hebling U., Heumann K., Hilbert H., Hillier L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Last sequer 28-FEB-2003 (Rel. 41, Last annote Beta-glucan synthesis-associated resistance protein 6).

KRE6 OR YPR159W.
                                                                                                                                                                                                                                                                                               MEDIINE-95176711; PubMed-7871892; Roemer T.D., Fortin N., Bussey H.; Roemer T.D., Fortin N., Bussey H.; "DNA sequence analysis of a 10.4 kbp region on the right arm chromosome XVI positions GPH1 and SGV1 adjacent to KRE6, and identifies two novel tRNA genes."; Yeast 10:1527-1530(1994).
   Urrestarazu L.A., Ushinsky S., Vierendeels F., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wezhong W.W., Zollner A., Vo D.H., Hani J.;
                                                                                                                                                                                                                                     STRAIN=S288c / AB972;
MEDLINE=97313271; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                   "Yeast beta-glucan synthesis: KRE6 encodes a predicted membrane protein required for glucan synthesis in vivo synthase activity in vitro.";
Proc. Natl. Acad. Sci. U.S.A. 88:11295-11299(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=92107936;
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NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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27, Last sequence up
41, Last annotation
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PRC1 Pathway and eactive 1. J. Cell Biol. 127:567-579(1994).

J. Cell Biol. 127:567-579(1994).

-i- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND (1->3)-BETA-D-GLUCAN POLYMERS OF THE YEAST CELL WALL IN VITYO. IT IS REQUIRED FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO. IT MAY BE A FORF FULL ACTIVITY OF BETA-GLUCAN SYNTHASE OR PETMA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN SYNTHASE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fc entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roemer T., Paravicini G., Payton M.A., Bussey H.; "Characterization of the yeast (1-->6)-beta-glucan biosynthetic components, Krefp and Sknlp, and genetic interactions between the PKCl pathway and extracellular matrix assembly.";
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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Interpro; IRR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase)
(1,3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X57094; CAA40379.1; PIR; S19012; S19012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as use by non-profit institutions as long as is modified and this statement is not removed. Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-ATCC 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paenibacillus polymyxa (Bacillus polymyxa).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUB_PAEPO 
P45797;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92041687; PubMed=1938968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1406;
    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650
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                                                 82
                                                                                         84
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                                                                                                                                                                                    25
                                                                                                                                                                                                                                 l Similarity
62; Conser
THGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDIIETIGNRDFKNTGGEFLGI 202
                                                                                                                                                             HIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGAN-SFVRDGKLFIKPTLLADNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VMSIDYVRIYQ
                                                                                                                                     NVFW-EPLSYFNSSTWQ---KADGYSNGQMFNCTWRANNVNFTNDGKLKLSLTSPANN--
                                                                                      PQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSARVRTFQKYSF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAMQVDYIRVYK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKALHPDG--NIGWRRISKEPMSIILNLGISNNWAYIDWQYIFFPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PDGCINRGGDPALQKPWS------NGDW-YNDAMRKFFDARGNWKWTWDDEGDN 370
                                                                                                                                                                                                                                                                                                                   27
129
133
56
238 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosidase;
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                                                                                                          238
129
133
85
26919
                                                                                                                                                                                                                                                    4.7%;
22.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal
                                                                                                                                                                                                                                                                                                                        WW.
                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                            Score 106; DE Pred. No. 0.09
                                                                                                                                                                                                                                                                                                                                         BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                      COCF7B4EA5D40E8C CRC64;
                                            -GEYRSTNNYG-YGLYEVSMKPAKNTGIVSSFFTYTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
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                                                                                                                                                                                                                                                  ; DB 1
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                                                                                                                                                                                                                                                                       1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                            96;
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                                            121
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DHET_ACEBU
DHET_ACEBU
ID DHET_AS
AC Q44002
AC Q44002
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 15-DEC
DT 28-FEB
DE Alcoho
GN ADH.
OS Acetob
OC Acetob
OC Acetob
CC -!- CO
RRA Thurne
RL Submitt
CC -!- CA
CC -!- SU
CC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
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Query Match
Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q44002; 0079:
15-DEC-1998 |
15-DEC-1998 |
28-FEB-2003 |
                                                                                             CHAIN
DOMAIN
BINDING
BINDING
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001479; Bac_PQQ.
InterPro; IPR002372; Bac_PQQ_repeat.
InterPro; IPR000345; CytC_heme_bind.
Pfam; PP01011; Bacterial_PQQ; 3.
SMART; SM00564; PQQ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reduced acceptor.

1. COFACTOR: PQQ AND HEME (BY SIMILARITY).

1. SUBUNIT: HETEROTETRAMER (DEHYDROGENASE, CYTOC SMALLER UNKNOWN SUBUNITS) THAT FORMS THE ALCO COMPLEX (BY SIMILARITY).

2. SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases -i- CATALYTIC ACTIVITY: A primary alcohol + acceptor - a
                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                   Oxidoreductase;
                                                                                                                                                                                                                                                                                            PROSITE; PS00363; BACTERIAL_PQ0_1; 1.
PROSITE; PS00364; BACTERIAL_PQ0_2; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y09480; CAA70688.1;
HSSP; Q9Z4J7; 1FLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entitles requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPACE (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE BACTERIAL POO DEHYDROGENASE FAMILY.
-!- SIMILARITY: Contains 1 cytochrome c domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thurner C.A.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DES11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetobacteraceae; Gluconacetobacter. NCBI_TaxID=33995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcohol dehydrogenase [acceptor] precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHET_ACEEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobacter europaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X82894; CAA58066.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHTATTNIP----STPGKIMMNLWNGTGVDSWLGSYNGANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKMGSTMHWGPGWDDNRYWLTSLPKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENQALLDVPYPLIDANPWWVDFWEWG----KPWLPQYENDNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                               635
651
654
655
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                                                                                35
739
739
651
655
80944
                                                                                                                                                                                                                                                                PQQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6160;
                      4.78;
                                                                                                                                                                                                                                                                        Heme;
                                                                                                  WW;
                                                                                                                                                                                                                                                                     Periplasmic;
                      Score 106; DB Pred. No. 0.34;
                                                                                             HEME (COVALENT) (BY SIMILARITY).
HEME (COVALENT) (BY SIMILARITY).
IRON (HEME AXIAL LICAND) (BY SIM
E681BB237ACB91F4 CRC64;
                                                                                                                                                                                            ALCOHOL DEHYDROGENASE [ACCEPTOR].
CYTOCHROME C-LIKE.
                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TQW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.
                                                                                                                                                                                                                                                                   Membrane;
                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOCHROME, AND TWO E ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DEIDI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1.99.8).
                                             Length 739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE PERIPLASMIC
                                                                                                                                                                                                                                                                signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294
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                                                                                                                      SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
MBL outstation –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            way
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78;

Conservative

37;

Pred. No. 0.3 7; Mismatches

118;

Indels

146;

Gaps

20;

Similarity

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RESULT 12
OSTA_HAEIN
ID OSTA_HAEIN
AC P44846;
DT 01-NOV-1995
DT 01-NOV-1995
DT 01-NOV-1995
DT 028-FEB-2003
DE OFGANIC SOLI
GN IMP OR OSTA
OS HAEMOPHILUS
OC PASTEUVIELLA
OX NCBI_TAXID=
RN [1]
RP SEQUENCE FR
STRAIN=Rd /
RX MEDLINE=953
RA Fleischmann
RA Kcrlavage A
RA Kcrlavage A
RA Kcrlavage A
RA Kcrlavage A
RA Grett J.D.
RA Gnehm C.L.
RA Fine L.D.
RA Gnehm C.L.
RA Fine L.D.
RA Gnehm C.L.
RA Gray C.
RO JENTIFICATI
RA Langen H.
RA Gray C.
RA Gray C.
SIMILAR
CC -i- SUBCELLI
CD -i- 
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                                                                                                                                                                                                                                                                                                                                Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick McKenney K., Sutton G., Fitzhugh W., Fleids C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen J.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                  Gray C., Fountoulakis M.;

"Two-dimensional map of the proteome of Haemophilus influenzae.

"Electrophoresis 21:411-429(2000).

-i-FUNCTION: Determines N-bexane tolerance. Involved in outer membrane permeability. Essential for envelope biogenesis. C part of a targeting/usher system for outer membrane compone
                                                                                                                                                                                                             MEDLINE-20137488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurellaceae;
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMP OR OSTA OR HI0730.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Rd / KW20 /
MEDLINE-95350630; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                 IDENTIFICATION BY
                              similarity).
SUBCELLULAR LOCATION: Outer
SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                     le-genome
     SWISS-PROT
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                                                                                                                                                                     n., Takacs B., Evers S.,
, Fountoulakis M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNFHFILN -- - VAVGGTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFAAMAFSP-----KTGLVYIPAQQVPFLYTNQVGGFTPHPDSWNLGLDMNKVGIPDSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGSIVALKPETGEYVWHFQETPMDQWDFTSVQQIMTLDLPINGETRHVIVHAPKNGFFYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDAKTGEFISGKNYVYVNWASGLDPKTG-----RPIYNPDALYTLTGKEWYGIPGDLGGH
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                                                                                                                                                                                                                                                                                                random sequencing
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32, Last sequence up
41, Last annotation
                                                                                                                                                                                                           MASS SPECTROMETRY.
PubMed-10675023;
                                                                                                                                                                                                                                 MASS
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   31
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 copyright.
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                                    membrane (By s
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                                                    similarity).
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                                                                                    biogenesis. Coulombrane components
through a
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 RESULT 13
XYND_RUMFL
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Best Local s
Matches 83
                                                                                                                                                                                                                                                                                                XYND_RUMFL Q53317;
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                           XYND
                                                                                                      NCBI_TaxID=1265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_01411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                       336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane; Signal; SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r; MF_01411; -; 1.
rPro; IPR005653; OstA.
rPro; PF03968; OstA; 1.
rPr04453; OstA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G64157; G64157; HI0730; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDYFDGAKWQHEVTATGGGNSEFQLYTQDG--ANS---FV-RDGKLFIKPTLLADNINPQ
                                                                                                                                                                                                                                                                                                                    MWHARFKIHGVPVFYTPYLQLPIGDRRRSGLLIPSAGTSSQDGLWYAQPIYWNIAPNYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPAMSA-RVRTFQKYSFT-
LDFNYHKYDLANGWLNFKLHSQAVR--FD
                                 ------LOKPWSNGDWYNDAMRKFFD
                                                                                                                                                                                               SLPKHSDDWNYGDNFHTFWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWE-WG
                                                                                                                                                                                                                                       TFTPKYMSRRGWQANGEFRYLTSIGE--
                                                                                                                                                                                                                                                                  ---PEDWYYGGWPRSGEIDIIETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLT
                                                                                                                                                                                                                                                                                                                                                            --HGRVVVHA-----
                                                                             RSTDGYANQY - - -
                                                                                                                  KP---WLPQYENDNPWAGGTNLAPFDQNFHFILNVAVGGTNGF-IPDGCINRGGDPA---
                                                                                                                                                          -- KRHLFYWNHNSSFLQNW
                                                                                                                                                                                                                                                                                                                                                                                                 -----GDNAWAVDASEIRQYVKEEYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.7%;
21.3%;
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                                                                             -- ARIAYYQPNYNFSLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                            -KMPVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANIC SOLVENT TOL
; E73C8A5786B02D1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                     -GKVAGEYLG-----KVRYSEYASDNR----
                                   355
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                                                                                                                                                            RLNINYTRVSDKRYFNDFDSIYG
                                                                             -AHQFQIFDDIVNIGPYRAVPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                          -DWLW---PAIWML----
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NND_RUMFL STANDARD; PRT; 802 AA.

XND_RUMFL STANDARD; PRT; 802 AA.

Q53317;

01-NOV-1997 (Rel. 35, Created)

10-NOV-1997 (Rel. 35, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update)

Xylanase/beta-glucanase precursor [Includes: Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase); Endo-beta-1,3-1,4 glucanase (EC 3.2.1.73)

XYND.

Ruminococcus flavefaciens.

Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae;

Ruminococcus.

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  Query Match
Best Local S
Matches 58
  InterPro; IPR001137; Glyco_hydro_11.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF02018; CBM_49; 1.
Pfam; PF004057; Glyco_hydro_11; 1.
Pfam; PF00722; Glyco_hydro_16; 1.
Pfam; PF007721; GLYCO_hydro_16; 1.
PRINTS; PR00911; GLHYDRIASE16.
PRINTS; PR009737; GLHYDRIASE16.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
Xylan degradation; Hydrolase; Glycosidase;
   ACT_SITE
ACT_SITE
ACT_SITE
  DOMAIN
DOMAIN
   DOMAIN
DOMAIN
   CHAIN
   EMBL;
  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  This
   SEQUENCE
   DOMAIN
   DOMAIN
   DOMAIN
   SIGNAL
  use by non-profit institutions as long
   PI- CATALYTIC ACTIVITY: Endohydrolysis
   J. Bacteriol. 175:2943-2951(1993)
  glucanase domains, encoded
flavefaciens.";
  InterPro;
  HSSP;
  between
  G (FAMILY 11 OF GLYCOSYL HYDROLASES). SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO
  GLYCOSYL HYDROLASES.
   557
   SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
    275
                                       703
  153
  S61204; AAB26620.1;
P23904; 1AJK.
  95
   Similarity
  MYNGVLDVWAMYGACTNTDNN--GCYRTGAAGDIPPAMSARVRTFQKYSFTHGRVVVHAK
                                     GKHEKLYDLGFDSSEAYHTYGFDWQPNYIAWYVDGREVYRATQDIPKTPGKIMMNAWPGL
  MPVGDWLWPAIWMLPEDWVYGG-----WPRSGEIDIIETIGNRDFKNTGGEF----
  FYHYGYYECSMQAMKNDGVVSSFFTYTGPS-DDNPWDEIDIEILGKNTTQVQFNYYTNGQ
   ------LGIQKMGST-----MHWGPGWDDN--
   MHGGYRDL----GTPMNTSATMISDFRTGKAGDF-----
  ----WVDFWEWGKPWLPQY
  PKHSDDWNYG----DNFHTFWFDWSPNGLRFFVDDEN--QALLDVPYP--LIDANPW---
  -PFDCW----
  IPR003305; CBM_CenC
   802
  Conservative
   AA;
   enzyme.
   5533
5533
5533
5533
5533
5543
5543
  ·WYKRNAVINDGCLQLSIDQKWTNDKNPD·----WDPRYSGGEFRTNN
  89091 MW;
   4.7%;
   .•
  26;
   CATALYTIC
   Λq
   POLY-THR.
POLY-THR.
POLY-THR.
   POTENTIAL.
XYLANASE/BETA-GLUCANASE.
A (XYLANASE).
B.
   LINKER.
C (BETA
   Pred.
   Score 105;
   C (BETA-GLUCANASE).
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
  Glycosidase;
   the xynD gene of Ruminococcus
  2880A689647284AF CRC64;
  Mismatches
  No.
  DOMAINS
   1,4-beta-D-glycosidic linkages
and 1,4-bonds.
   0
   of
   There
  .44;
   DB 1;
   --
-ENDNPW
  here are no res
   1,4-beta-D-xylosidic
  Signal;
  BELONGS
  83;
  WITH XYLANASE AND
   Length
295
  Indels 112;
  or
   -FASDGWINGK----
   restrictions
  FAMILY
  CELLULASE
   802;
   tha collaboration -
  16
   -RYWLTSL
  ENDO-
  Gaps
  얽
  FAMILY
  no
   g
  152
  274
  643
  199
   596
  702
   225
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                      Qγ
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   δδ
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  δõ
   RESULT 14
GUB_BACAM
  밁
  Matches
  Query Match
Best Local
   ACT_SITE
DISULFID
   "The beta-glucanase gene from Bacillus am extensive homology with that of Bacillus Gene 49:177-187(1986).
   SEQUENCE
   InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
PRINTS; PR00737; GLHYDRLASE16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16;
   EMBL; M15674; AAA87323.1;
PIR; A29091; A29091.
HSSP; P27051; IGBG.
  entities requires a license agreement (S or send an email to license@isb-sib.ch).
  use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
  use
  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
  -i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages in beta-D-glucans containing 1,3- and 1,4-bonds.
-i- MISCELLANEOUS: BETA-GLUCANASES OF BACILLUS HAVE A SUBSTRATE RANG SIMILAR TO LICHENASE OF GERMINATING BARLEY.
-i- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
  GUB_BAC
P07980;
   CHAIN
   Bacillus amyloliquefaciens.
Bacteria; Firmicutes; Bacil
   BGLA
  the European Bioinformatics Institute.
   STRAIN=BE 20/78;
MEDLINE=87192007; PubMed=3106158;
  Ol-AUG-1988 (Rel. 08, Last sequence update)
Ol-JUN-1994 (Rel. 29, Last annotation update)
Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4
[1_3-1,4-beta-D-glucan 4-glucanohydrolase) (Lichenase).
   01-AUG-1988
01-AUG-1988
  SIGNAL
   Hydrolase;
  SEQUENCE FROM
  NCBI_TaxID=1390;
  BACAM
   130
 157
  184
   763 TVDDWLKAFNGRTPLTAHYQWVTYNKNGVQHSSQGQNPW
  99
   8
   12
   71
  Similarity
53; Conser
FADLGFDAANAYHTYAFDWQPNSIKWYVDGQLKHTATTQIP
   IETIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDD
  MSARVR-----TFQKYSFTHGRVVVHAKMPVGDWLWPAIWMLPEDWVYGGWPRSGEIDI
  LFIKPTLLADNINPQTGAPFGTDF-MYNGVLDVWAMYGACTNTDNNGCYRTGAAGDIPPA 129
                         DDWNYG---
  LYEVRMKPAKNTGIVSSFFTYTGPTE--GTPWDEIDIEFLGKDTTKVQFNYYTNGAGNHE
  SLGEMRLALTSPSYNKFDCGENRSV-
   LFMSLCGITSSVSAQTGGSFFEPFNSYNSGL--WQKADGYSNGDMFNC--TWRANNVSMT
   134
57
239 AA;
   Glycosidase;
  Conservative
  (Rel.
  N.A.
  STANDARD;
  25
239
134
86
26928
  , 80
                        DNFHTFWFDWSPNGLRFFVDDE--NQALLDVPYPLIDANPWWVDFWEWG-
  4.7%;
  Created)
  Bacillales;
  Signal.
   ¥.
   31;
   Score 104.5;
Pred. No. 0.13
31; Mismatches
   BETA-GLUCANASE.
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
; A76A64268A7AAAOB CRC64;
   Bacillaceae;
   (See
  Knowles J.;
s amyloliquefaciens
lus subtilis.";
  239
   ۳.
  There are no restrictions
  .13;
  A
  as its content
   DB 1;
  http://www.isb-sib.ch/announce/
  100;
   Usage
   Bacillus
   801
  Indels
  Length
   Ьy
  -QTYGYG------
   and
 AAPGKIMMNLWNG
  -NRYWLTSLPKHS
  239;
  shows
  glucanase)
  a collaboration -
   71;
   for
   'n
  Gaps
  RANGE
   n no way
   9
                        282
   229
  183
   156
   98
  67
   its
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TGVDDWLGSYNGVNP 226 ---KPWLPQYENDNP

294

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RESULT 15
KRE6_CANAL
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  В
   Query Match
Best Local S
Matches 78
   KRE6_CANAL
P87023;
01-NOV-1997
01-NOV-1997
28-FEB-2003
  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
  DOMAIN
DOMAIN
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   "Isolation of the Candida albicans homologs of Saccharomyces cerevisiae KRE6 and SKN1: expression and physiological function.";
J. Bacteriol. 179:2363-2372(1997).
-i- FUNCTION: INVOLVED IN THE SYNTHESIS OF (1->6)- AND (1->3) BETA-D-GLUCAN POLYMERS OF THE YEAST CELL WALL IN VITO. IT IS REQUIRED FOR FULL ACTIVITY OF BETA-GLUCAN SYNTHASE IN VITRO. IT MAY BE A BETA-GLUCAN SYNTHASE, PART OF A MULTIPROTEIN GLUCAN SYNTHASE OR
  InterPro; IPR005629; DUF338. Pfam; PF03935; DUF338; 1.
  Eukaryota; Fungi; Ascomycota; Saccharomycetales; mitosporic
  DOMAIN
   Mio T.,
  MEDLINE=97234650;
   SEQUENCE FROM
  Candida albicans (Yeast)
   Beta-glucan synthesis-associated protein KRE6.
  SEQUENCE
  DOMAIN
  DOMAIN
   TRANSMEM
   DOMAIN
   EMBL; D88490; BAA19593.1; -
  Yamada-Okabe H.;
  A MODULATOR.
SUBCELLULAR LOCATION:
SIMILARITY: STRONG, TO
                                     347
   MODULATOR
              08
  20
  78;
  Similarity
   Yamada-Okabe
DNINPQTGAPFGTDFMYNGVLDV-WAMYGACTNT------DNNGCYRTGAAGDI 126
                                    DGSEWVLVFSDEFD-----
   DWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQDGANSFVRDGKLFIKPTLLA
   486
568
593
721
740
  (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
   Conservative
   N.A.
  Transmembrane;
  ă,
   740
46
56
134
1147
201
399
445
486
568
5721
82456 MW;
   STANDARD;
  PubMed=9079924; abe T., Yabe T.,
   4.68;
17.18;
  TO
  Type II membrane protein. Golgi.
  48;
  SKN1.
   N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT
   Score 103.5;
Pred. No. 0.54
18; Mismatches
  POLY-ASN.
POLY-GLY.
POLY-SER.
  POLY-GLU.
POLY-SER.
   Cell wall; Golgi stack; Signal-anchor. CYTOPLASMIC (POTENTIAL).
   CYTOPLASMIC (PÓTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
   (POTENTIAL).
LUMENAL (POT
   Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
  PRT;
   Nakajima T., Arisawa
  740
  (POTENTIAL).
   ; DB
.54;
   ₽.
   126;
   1;
                                    --AEGRTFYEGDDQFFTAP----
   Length 740;
   Indels
  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
   .
.
  203;
   Gaps
                                     377
   79
   19;
```

| Qу<br>Db                                                                                                          | Оy                                                                   | Оу<br>Оъ                                                             | ОУ                                                                                    | ОУ                | Qy                                                                              | Db                                             |
|-------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------------------------------------------|-------------------|---------------------------------------------------------------------------------|------------------------------------------------|
| 349<br>657                                                                                                        | 289<br>627                                                           | 229<br>594                                                           | 186<br>534                                                                            | 177<br>474        | 127<br>420                                                                      | 378                                            |
| 349 AMRKFFDARGNWKW-TWDDEGDNNAMOVDYIRVYK 382<br>:    :   : ::  :  :<br>657 -LILNLGISNNWAYIDWPSISFPVTFRIDYVRVYQ 690 | 289 YENDNPWAGGTNLAPFDONFHFILNVAVGGTNGFIPDGCINRGGDPALQKPWSNGDWYND 348 | SDDWNYGDNFHTEWFDWSPNGLRFFVDDENQALLDVPYPLIDANPWWVDFWEWGKPWLPQ 288   : | TIGNRDFKNTGGEFLGIQKMGSTMHWGPGWDDNRYWLTSLPKH 228 :   :   :   :   :   :   :   :   :   : | 177 RSGEIDIIE 185 | PPAMSARVRTEQKYSFTHGRVVVHAKMP-VGDWLWPAIWMLPEDWVYGGWP 176  ::::     ::   ::     : | DIHYDATKDLEWYDPDAVTTANGTLNLRMDAYKNHNLFYRSG 419 |
|                                                                                                                   | or co                                                                | yı do                                                                | w w                                                                                   | w 01              | ωσ                                                                              | Ü                                              |

Search completed: September 16, Job time: 30.0831 secs 2003, 11:26:31

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Result
No.
  Database
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Minimum DB
Maximum DB
   Total number of hits satisfying chosen parameters:
  Title:
Perfect score:
  Searched:
   OM protein - protein search, using sw model
  Scoring table:
  Sequence:
   Run on:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                          716.5
713
703
601
596.5
417
413.5
390.5
369.5
   seq length: 0 seq length: 2000000000
  Query
Match
    100.0
90.3
34.9
32.0
31.8
31.8
31.4
26.6
18.5
18.5
15.8
15.8
   SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria
   830525 seqs, 258052604 residues
   BLOSUM62
Gapop 10.0 , Gapext 0.5
   September 16, 2003, 11:22:17; Search time 118.005 Seconds (without alignments) 839.729 Million cell updates/sec
   9:
10:
11:
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14:
16:
16:
  1 MRWTLVVLCLLFGEGFAFTD......DDEGDNNAMQVDYIRVYKRN 384
   US-09-596-101C-3
2240
   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
  sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
  sp_rodent:*
sp_virus:*
   sp_phage: *
  sp_mammal:*
   sp_archea:*
sp_bacteria:*
   sp_organelle:*
   sp_mhc:*
  sp_invertebrate:*
  sp_human:*
  sp_fungi:*
   sp_vertebrate: *
   sp_plant:*
  Length
    462
371
533
278
495
495
877
492
1321
  384
382
376
366
395
   DB
  Q96TU5
Q9NL89
   Q26660
Q17492
Q9C236
Q8T9V2
  077072
Q95VY3
   Q9VVR5
Q59328
O52754
   Q8MVS9
Q8NON3
Q9UOG4
                                     Q45095
   Ħ
   SUMMARIES
  830525
Q8t9v2 aedes aegyp
Q8cw17 vibrio vuln
Q96tu5 alternaria
Q9n189 bombyx mori
Q45095 bacillus ci
Q9vvr5 drosophila
Q59328 clostridium
Q52754 rhodothermu
  077072 eisenia foe
095vy3 lumbricus t
08mvs9 litopenaeus
08n0n3 penaeus mon
09u094 pacifastacu
026660 strongyloce
017492 anopheles g
09c236 neurospora
   Description
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| 4                 | 4                  | 43     | 42                | 41     | 40     | 39     | 38     | 37                | 36                | 35     | 34                 | 33                | 32                 | 31     | 30                 | 29     | 28     | 27     | 26                 | 25     | 24                 | 23     | 22     | 21                 | 20                 | 19                 | 18                 | 17 ·               |
|-------------------|--------------------|--------|-------------------|--------|--------|--------|--------|-------------------|-------------------|--------|--------------------|-------------------|--------------------|--------|--------------------|--------|--------|--------|--------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 209               | 239                | 240    | 247               | 248.5  | 249.5  | 249.5  | 249.5  | 257.5             | 262.5             | 263    | 275.5              | 284               | 286.5              | 287    | 290.5              | 295    | 295    | 302    | 307                | 312.5  | 314                | 323    | 326.5  | 329.5              | 333.5              | 340                | 350                | 350                |
| 9.                | 10.7               |        | 11.0              | 11.1   | 11.1   | 11.1   | 11.1   | 11.5              | 11.7              | 11.7   | 12.3               | 12.7              | 12.8               | 12.8   | 13.0               | 13.2   | 13.2   | 13.5   | 13.7               | 14.0   | 14.0               | 14.4   | 14.6   | 14.7               | 14.9               | 15.2               | 15.6               | 15.6               |
| 6/3               | 422                | 254    | 383               | 452    | 461    | 432    | ,410   | 297               | 297               | 458    | 285                | 642               | 422                | 646    | 752                | 490    | 490    | 481    | 306                | 411    | 467                | 494    | 488    | 487.               | 565                | 482                | 435                | 301                |
| U                 | 16                 | Ν      | N                 | 16     | Ç      | Ç      | σı     | سو                | 17                | 16     | 16                 | 16                | N                  | N      | N                  | G      | տ      | u      | N                  | N      | σ                  | UI     | ப      | Մ                  | N                  | ű                  | 2                  | 16                 |
| Z8072Ö            | Q9EWR5             | Q8GCZ7 | Q8GCZ5            | Q8PBD4 | Q9VVR4 | Q8IQT7 | Q8IQT6 | 073951            | Q8U4K8            | Q8PMZ0 | Q9F3A0             | Q9WXN1            | Q9ZG90             | Q60039 | Q8GRB5             | Q9NHA8 | Q9VSR4 | 096363 | Q51333             | Q8KKH3 | Q17233             | Q9NHB0 | Q8MU95 | Q9NJ98             | Q8GRB4             | Q8ISB6             | 068641             | Q9AB54             |
| Q2/082 tachypieus | Q9ewr5 streptomyce |        | Q8gcz5 lysobacter | 4      |        |        |        | 073951 pyrococcus | Q8u4k8 pyrococcus |        | Q9f3a0 streptomyce | Q9wxn1 thermotoga | Q9zg90 flavobacter |        | Q8grb5 pseudomonas |        |        |        | Q51333 oerskovia x |        | Q17233 bombyx mori | _      |        | Q9nj98 manduca sex | Q8grb4 pseudomonas | Q8isb6 manduca sex | O68641 oerskovia x | Q9ab54 caulobacter |

## ALIGNMENTS

| RESULT 1  O77072  PRELIMINARY; PRT; 384 AA.  AC 077072; PRELIMINARY; PRT; 384 AA.  COT7072; PREMBLrel. 08, Last sequence update)  DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  DE CCF1.  COC Lumbricina; Comment of the sequence update)  COT Lumbricina; Lumbricidae; Eisenla.  COC Lumbricidae; Eisenla.  COC Lumbricidae; Eisenla.  COL Lumbricina; Lumbricidae; Eise |                                                              |                                                                                                                                    |                   |                                                                        |                            |                                                                                  |                                                               |                                                                 |                                                               |                                                              |                                  |                   |   |                 |                                                                                                      |                                                            |      |                   |                 |                 |                      |                     |                    |        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------|-------------------|------------------------------------------------------------------------|----------------------------|----------------------------------------------------------------------------------|---------------------------------------------------------------|-----------------------------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------|----------------------------------|-------------------|---|-----------------|------------------------------------------------------------------------------------------------------|------------------------------------------------------------|------|-------------------|-----------------|-----------------|----------------------|---------------------|--------------------|--------|
| PRELIMINARY; PRT; 384 AA.  998 (TrembLrel. 08, Created) 998 (TrembLrel. 18, Last sequence update) 001 (TrembLrel. 18, Last annotation update) cytolytic factor 1.  60etida (Common brandling worm) (Common dung-worm). a; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; na; Lumbricidae; Eisenia.  10=6396;  FROM N.A.  10=6396;  FROM N.A.  10=6396;  FROM N.A.  10=10 M., Hanssens F., Raymakers J., Van Dyck E., 10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=6396;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10=64;  10= | oy Oy                                                        | Query<br>Best<br>Match                                                                                                             |                   |                                                                        |                            |                                                                                  |                                                               |                                                                 |                                                               |                                                              |                                  |                   |   |                 |                                                                                                      |                                                            | _    |                   |                 |                 |                      | AC 07               | 17 C1              | RESULT |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | MRWTLVVLCLLEGEGFAFTDWDQYHIVWQDEFDYFDGAKWOHEVTATGGGNSEFQLYTQD | 100.0%; Score 2240; DB 5; Length 384;<br>Similarity 100.0%; Pred. No. 1.9e-167;<br>4; Conservative 0; Mismatches 0; Indels 0; Gaps | 384 AA; 44322 MW; | nterro; rekuuu/5/; Giyco_nydro_16.<br>fam; PF00722; Glyco_hydro_16; 1. | MBL; AF030028; AAC35887.1; | CLIVACION OI Prophenoloxidase cascade.";<br>. Biol. Chem. 273:24948-24954(1998). | inding protein from Eisenia foetida earthworm involved in the | Identification and cloning of a glucan- and Lipopolysaccharide- | evets H., Brys L., Gomez J., De Baetselier P., Timmermans M., | eschin A., Bilei M., Hanssens F., Raymakers J., Van Dyck E., | EDLINE-98406152; PubMed-9733802; | EQUENCE FROM N.A. | 1 | CBI TAXID=6396; | ukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Hapiotaxida;<br>umbricina: Tumbricida: Eiconia | isenia foetida (Common brandling worm) (Common dung-worm). | CF1. | tolytic factor 1. | (TrEMBLrel. 18, | (TrEMBLrel. 08, | 1998 (TrEMBLiel, 08, | - FARBURANCE - FALL | DOFT TWINDOV. DOM. |        |

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RESULT

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  В
   Query Match
Best Local S
Matches 346
   Signal.
SIGNAL
  Beschin A., De Baetseller P., Bilej M.;
"Distinct carbohydrate recognition domains of an earthworm complex in the recognize Gram negative and Gram positive bacteria. Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF395805; AAL09587.1; .
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JDC-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Coelomic cytolytic factor precursor.
Lumbricus terrestris (Common earthworm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
  Q95VY3
  NCBI_TaxID=6398;
   Q95VY3;
01-DEC-2001
  SEQUENCE
  EQUENCE FROM N.A.
   361
  361
  301
   301
  241
  241
   181
  181
   121
299
                                 301
   181
  181
   121
   121
   121
   al Similarity
346; Conser
  61
   61
  ب
   MRWTLVVLCLLFGEGFAFTDWDQYHIVWQDEFDYFDGAKWQHEVTATGGGNSEFQLYTQD
   KWTWDDEGDNNAMQVDYIRVYKRN
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   GANSFVRDGKLFIKPTLLADNINPQTGAPFGTDFMYNGVLDVWAMYGACTNTDNNGCYRT
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   01-OCT-2002
01-OCT-2002
01-MAR-2003
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01-OCT-2002
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01-MAR-2003
   ROUX M.M., Pain A., Klimpel K.R., Dhar A.K.;
"The Lipopolysaccharide and beta-1,3-Glucan Binding Prote
Opregulated in White Spot Virus-Infected Shrimp (Penaeus
stylirostris).";
J. Virol. 76:7140-7149(2002).
EMBL; AF473579; AAM73871.1; -.
InterPro; IPR000757; Glyco_hydro_16.
Pfam; PF00722; Glyco_hydro_16; 1.
SEQUENCE 376 AA; 42610 MW; D7ADC5A310208885 CRC64;
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43.0%;
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  106;
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   Protein
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  44;
   Gene
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RESULT OF STREET  δÃ
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Matches 159
   Q9U0G4 PRELIMINARY; PRT; 361 AA.
Q9U0G4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-CT-2001 (TrEMBLrel. 18, Last annotation update)
  Eukaryota; Metazoa; Arthropoda; Crustacea; Malace
Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Astacoidea; Astacidae; Pacifastacus.
Lee S., Wang R., Soderhall K.;
"A lipopolysaccharide- and beta-1,3-glucan-binding protein fr.
hemocytes of the freshwater crayfish Pacifastacus leniusculu:
purification, characterization, and cDNA cloning.";
J. Biol. Chem. 275:1337-1343(2000).
  Submitted
EMBL; AF36
  TISSUE-Hemocyte;
MEDLINE-20092910; PubMed-10625682;
   Lipopolysaccharide LGBP.
   Sritunyalucksana K.,
"The beta-1,3-glucan
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  NQYGGTTLHWGPFWPYNFFEKTHAEYSANTGSFADDFHVWRLDWTKDNMEFYVDDVLQLT
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   34.9%;
ilarity 43.3%;
Conservative 5
  360
   382
  and
  Lee S.Y.
binding
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Pred. No. 3.3e
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Crustacea; Malacostraca;
Oda; Dendrobranchiata; Pe
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179

LIFQEEFDSFNLDIWEHEMTAGGGGNWEFEYYTNNRSNSYVRDGKLFIKPTLTTDKL---

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  SQ SQ
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  01-NOV-1996 (TrEMBL)
01-NOV-1996 (TrEMBL)
01-DEC-2001 (TrEMBL)
Beta 1,3-glucanase.
  Q26660;
Q26660;
  Bachman E.S., McClay D.R.;

Molecular cloning of the first metazoan beta-1,3
of the sea urchin Strongylocentrotus purpuratus.";

Proc. Natl. Acad. Sci. U.S.A. 93:6808-6813(1996).

EMBL; U49711; AAC47235.1;
  Eukaryota; Metazoa; Echino
Echinoidea; Euechinoidea;
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; E
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Similarity 42.7%;
58; Conservative (
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  355
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No. 1
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InterPro; IPR000757; Glyco_hydro_16; 1.
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   MEDLINE=97470997; PubMed=9326640;
Dimopoulos G., Richman A., Mueller H.M., Kafatos F.C.;
"Molecular immune responses of the mosquito Anopheles of
bacteria and malaria parasites.";
Proc. Natl. Acad. Sci. U.S.A. 94:11508-11513(1997).
   Eukaryota; Metazoa; Arthi
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01-OCT-2001 (TrEMBLrel. 18, Last annotation updat
Putative GRAM negative BACTERIA binding protein p
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  Anopheles gambiae (African malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Thilte U., Aign V., Holy

Mewes H.W
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EMBL; AL513445; CAC28724.1; -
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SEQUENCE 462 AA; 51868 MW; 28808
   Schulte U., Aign V.,
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Submitted (FEB-2001)
   Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomy
Sordariales; Sordariaceae; Neurospora
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GN VV213
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01-MAR-2003 (TrEMBLE. 23, Last sequence update)
01-MAR-2003 (TrEMBLE. 23, Last annotation update)
VV21300.
   Ribeiro J.M.C.;

"Toward the sialome of the adult female mosquito Aedes aegypti.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; Ar466594; AAL76017-1;

EMBL; AR7601757; Glyco_hydro_16.

InterPro; IRR000757; Glyco_hydro_16; 1.

SEQUENCE 371 AA; 41943 MW; IFE2E5DC7B665CE6 CRC64;
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Aedes aegypti (Yellowfever mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2002 (TrEMBLrel. 22,
  VSTRAIN-Black eye; TISSUE-Salivary gland; Valenzuela J.G., Pham V.M., Garfield M.K.,
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  ---YGEAFLKSGVINLNEGPQSQRCTDAPGWAEQIHGCYRRGSPDRILNPVRSARLRTV
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Conservative 7
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AC 096TU
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 29,
01-MAR-2003 (TrEMBLrel. 20)
                           NON_TER
  Eshel D., Prusky D., Dinoor A.;
"Mixed'linked glucanase precursor of Alternaria alternata.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282319; AAK69516.1;
Interpro; IPR000757; Glyco_hydro_16.
PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
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Alternaria alternata.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
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Query Match

18.5%;

Score 413.5;

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Length

278;

Best Local

Similarity

33.6%;

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01-OCT-2000 (TrembLrel. 15, Last sequence update)
01-JUN-2002 (TrembLrel. 21, Last annotation update)
Beta-1,3-glucan recognition protein precursor.
Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycidae; Bombyx.
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SIGNAL
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STRAIN-Kinshu x Showa; TISSUE-Hemocyte;
MEDLINE-20138243; PubMed-10671539;
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   silkworm,
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:| ||| ||| || : | : : : :
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BETA-1,3-GLUCAN RECOGNITION PROTEIN

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Matches 103;
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INTERPRO : IPR003343; Big_2.
InterPro; IPR000757; Glyco_hydro_16.
INTERPRO : IPR003599; Ig.
   Yamamoto M., Aono R., Horikoshi K.;
"Structure of the 87-kDa beta-1,3-glucanase general translife and properties of the enzyme accumulates acceptated a coli carrying the gene.";
Biosch. Biocehnol. Biochem. 57:1518-1525(1993)
   Bacillus circulans.
Bacteria; Firmicutes;
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   Š
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23, Last annotation updat
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  Bacillaceae;
     GKFFFKVTRDQWYSAAAPNNP----
   ucanase gene
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   -WLKGTIMAPFDELFY
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   141;
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RA Addams M.D., Celniker S.E., Helt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Hichards S.A., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N.,
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RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.K.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherifi A.,
RA Melson D.R., Nelson K.A., Standers R.D.C., Scheeler F., Shen H.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reese M.G.,
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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Waissenbach J.,
RA Mang S.-Y., Wassarman D.A., Weinstock G.M., Wang X., Smith T.,
Sheng Y.-Y., Wassarman D.A., Weinstock G.M., Wang X., Smith H.O.,
RA Schelber R.M., Saunders R.D.C., Zhon Q., Zhon Q., Zhon Q., Zhon Q
  RESULT
Q9VVR5
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     Query Match
  The genome sequence of Drosophila Science 287:2185-2195(2000).
  Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hazapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2001 (TrEMBLrel.
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  5.
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   672
Q59328
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01-MAR-2003 (TrEMBLrel. 23, La
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                                   Zverlov V.V., Schwarz W.I
Submitted (FEB-2002) to
EMBL; 899732; CAR61884-2
EMBL; AJ307315; CAC27412
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  W.H.;
   Clostridia; Clostridiales; Clostridiaceae;
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(EC 3.2.1.6).
  67;
  EMBL/GenBank/DDBJ
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Search completed: September 16, 2003, 11:28:43 Job time: 121.005 secs
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